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NATURAL LIGAND OF G PROTEIN COUPLED RECEPTOR ChemR23 AND USES THEREOF

This application claims priority to US Provisional No: _____, filed 7/9/01.

FIELD OF THE INVENTION

The invention relates to the identification of the natural ligand for the orphan G-Protein Coupled Receptor (GPCR) ChemR23 and uses thereof.

BACKGROUND OF THE INVENTION

G-protein coupled receptors (GPCRs) are proteins responsible for transducing a signal within a cell. GPCRs have usually seven transmembrane domains. Upon binding of a ligand to an extra-cellular portion or fragment of a GPCR, a signal is transduced within the cell that results in a change in a biological or physiological property or behaviour of the cell. GPCRs, along with G-proteins and effectors (intracellular enzymes and channels modulated by G-proteins), are the components of a modular signaling system that connects the state of intra-cellular second messengers to extra-cellular inputs.

GPCR genes and gene products can modulate various physiological processes and are potential causative agents of disease. The GPCRs seem to be of critical importance to both the central nervous system and peripheral physiological processes.

The GPCR protein superfamily is represented in five families : Family I, receptors typified by rhodopsin and the beta2-adrenergic receptor and currently represented by over 200 unique members; Family II, the parathyroid hormone/calcitonin/secretin receptor family; Family III, the metabotropic glutamate receptor family, Family IV, the CAMP receptor family, important in the chemotaxis and development of *D. discoideum*; and Family V, the fungal mating pheromone receptor such as STE2.

G proteins represent a family of heterotrimeric proteins composed of α, β and γ subunits, that bind guanine nucleotides. These proteins are usually linked to cell surface receptors (receptors containing seven transmembrane domains) for signal transduction. Indeed, following

ligand binding to the GPCR, a conformational change is transmitted to the G protein, which causes the α-subunit to exchange a bound GDP molecule for a GTP molecule and to dissociate from the βγ-subunits.

The GTP-bound form of the α, β and γ-subunits typically functions as an effector-modulating moiety, leading to the production of second messengers, such as cAMP (e.g. by activation of adenyl cyclase), diacylglycerol or inositol phosphates.

Greater than 20 different types of α-subunits are known in humans. These subunits associate with a small pool of β and γ subunits. Examples of mammalian G proteins include Gi, Go, Gq, Gs and Gt. G proteins are described extensively in Lodish et al., *Molecular Cell Biology* (Scientific American Books Inc., New York, N.Y., 1995; and also by Downes and Gautam, 1999, The G-Protein Subunit Gene Families. *Genomics* 62:544-552), the contents of both of which are incorporated herein by reference.

Known and uncharacterized GPCRs currently constitute major targets for drug action and development. There are ongoing efforts to identify new G protein coupled receptors which can be used to screen for new agonists and antagonists having potential prophylactic and therapeutical properties.

More than 300 GPCRs have been cloned to date, excluding the family of olfactory receptors. Mechanistically, approximately 50-60% of all clinically relevant drugs act by modulating the functions of various GPCRs (Cudermann et al., *J. Mol. Med.*, 73:51-63, 1995).

ChemR23, also called Dez [Sequence ID Nos: 1 (human polynucleotide sequence, Fig. 1); 2 (human amino acid sequence, Fig. 2); 3 (mouse polynucleotide sequence, Fig. 3); 4 (mouse amino acid sequence, Fig. 3); 5 (rat polynucleotide sequence; Fig. 4); and 6 (rat amino acid sequence, Fig. 4)] has been described as an orphan G protein coupled receptor related to GPR-1 (38% overall amino acid identity), C3a receptor (38%), C5a anaphylatoxin receptor (36%) and formyl Met-Leu-Phe receptors (35%). ChemR23 is more distantly related to the chemokine receptors subfamily (Methner A, Hermey G, Schinke B, Hermans-Borgmeyer I. (1997) *Biochem Biophys Res Commun* 233:336-42; Samson M, Edinger AL, Stordeur P, Rucker J, Verhasselt V, Sharron M, Govaerts C, Mollereau C, Vassart G, Doms RW, Parmentier M. (1998) *Eur J*

Immunol 28:1689-700). ChemR23 transcripts were found to be abundant in monocyte-derived dendritic cells and macrophages, with or without treatment with LPS. Low expression can also be detected by reverse transcription-PCR in CD4+ T lymphocytes. In situ hybridization experiments also showed that the receptor was differentially regulated during development, with a prominent expression in developing osseous and cartilaginous tissues. It was also detectable in the adult parathyroid glands, indicating a possible function in phosphocalic metabolism.

The gene encoding ChemR23 was assigned by radiation hybrid mapping to the q21.2-21.3 region of human chromosome 12, outside the gene clusters identified so far for chemoattractant receptors. ChemR23 was tested in fusion assays for potential coreceptor activity by a range of HIV-1, HIV-2 and SIV viral strains. Several SIV strains (SIVmac316, SIVmac239, SIVmacl7E-Fr and SIVsm62A), as well as a primary HIV-1 strain (92UG024-2) efficiently used ChemR23 as a co-receptor. This receptor therefore appears to be a coreceptor for immunodeficiency viruses that does not belong to the chemokine receptor family. It is also a putative chemoattractant receptor and it could play an important role in the recruitment or trafficking of leukocyte cell populations.

TIG2 (Tazarotene-induced gene 2 [Sequence ID Nos: 7 (human TIG2 polynucleotide sequence, Fig. 6); 8 (human amino acid sequence, Fig. 6); 9 (mouse polynucleotide sequence, Fig. 7); and 10 (mouse amino acid sequence, Fig. 7)] was identified as a cDNA, the expression of which is up-regulated by the treatment of skin raft cultures by the retinoic acid receptor (RAR) beta/gamma-selective anti-psoriatic synthetic retinoid, tazarotene [AGN 190168/ethyl 6-[2-(4,4-dimethylthiochroman-6-yl)-ethynyl] nicotinate] (Nagpal S, Patel S, Jacobe H, DiSepio D, Ghosn C, Malhotra M, Teng M, Duvic M, Chandraratna RA. (1997) *J Invest Dermatol* 109: 91-5). The retinoid-mediated up-regulation in the expression of TIG2 was confirmed by Northern blot analysis. The TIG2 cDNA is 830 bp long and encodes a putative protein product of 164 amino acids. TIG2 is expressed and induced by tazarotene in culture only when keratinocytes and fibroblasts form a tissue-like 3-dimensional structure. RAR-specific retinoids were also shown to increase TIG2 mRNA levels. In contrast, neither RXR-specific retinoids nor 1,25-dihydroxyvitamin D3 increased TIG2 levels in these cells. TIG2 is also expresssed at high levels in nonlesional psoriatic skin but at lower levels in the psoriatic lesion and its expression is up-regulated in psoriatic lesions after topical application of tazarotene. In addition, TIG2 has been

shown to be dramatically upregulated by 1,25 dihydroxyvitamin D3 and dexamethasone in osteoclast-supporting stromal cells (Adams AE, Abu-Amer Y, Chappel J, Stueckle S, Ross FP, Teitelbaum SL, Suva LJ. (1999) *J Cell Biochem* 74: 587-95).

SUMMARY OF THE INVENTION

The invention relates to the identification of TIG2, the polypeptide product of Tazarotene-Induced Gene 2, as a natural ligand of the ChemR23 GPCR. The invention encompasses the use of the interaction of ChemR23 polypeptides and TIG2 polypeptides as the basis of screening assays for agents that modulate the activity of the ChemR23 receptor. The invention also encompasses diagnostic assays based upon the ChemR23/TIG2 interaction, as well as kits for performing diagnostic and screening assays.

The invention encompasses a method of identifying an agent that modulates the function of ChemR23, the method comprising: a) contacting a ChemR23 polypeptide with a TIG2 polypeptide in the presence and absence of a candidate modulator under conditions permitting the binding of the TIG2 polypeptide to the ChemR23 polypeptide; and b) measuring the binding of the ChemR23 polypeptide to the TIG2 polypeptide, wherein a decrease in binding in the presence of the candidate modulator, relative to the binding in the absence of the candidate modulator, identifies the candidate modulator as an agent that modulates the function of ChemR23.

The invention further encompasses a method of detecting the presence, in a sample, of an agent that modulates the function of ChemR23 in a sample, the method comprising a) contacting a ChemR23 polypeptide with a TIG2 polypeptide in the presence and absence of the sample under conditions permitting the binding of the TIG2 polypeptide to the ChemR23 polypeptide; and b) measuring the binding of the ChemR23 polypeptide to the TIG2 polypeptide, wherein a decrease in binding in the presence of the sample, relative to the binding in the absence of the candidate modulator, indicates the presence, in the sample of an agent that modulates the function of ChemR23.

In a preferred embodiment of either of the preceding methods, the measuring is performed using a method selected from label displacement, surface plasmon resonance, fluorescence resonance energy transfer, fluorescence quenching, and fluorescence polarization.

The invention further encompasses a method of identifying an agent that modulates the function of ChemR23, the method comprising: a) contacting a ChemR23 polypeptide with a TIG2 polypeptide in the presence and absence of a candidate modulator; and b) measuring a signaling activity of the ChemR23 polypeptide, wherein a change in the activity in the presence of the candidate modulator relative to the activity in the absence of the candidate modulator identifies the candidate modulator as an agent that modulates the function of ChemR23.

The invention further encompasses a method of identifying an agent that modulates the function of ChemR23, the method comprising: a) contacting a ChemR23 polypeptide with a candidate modulator; b) measuring a signaling activity of the ChemR23 polypeptide in the presence of the candidate modulator; and c) comparing the activity measured in the presence of the candidate modulator to the activity measured in a sample in which the ChemR23 polypeptide is contacted with a TIG2 polypeptide at its EC_{50}, wherein the candidate modulator is identified as an agent that modulates the function of ChemR23 when the amount of the activity measured in the presence of the candidate modulator is at least 50% of the amount induced by the TIG2 polypeptide present at its EC_{50}.

The invention further encompasses a method of detecting the presence, in a sample, of an agent that modulates the function of ChemR23, the method comprising: a) contacting a ChemR23 polypeptide with TIG2 polypeptide in the presence and absence of the sample; b) measuring a signaling activity of the ChemR23 polypeptide; and c) comparing the amount of the activity measured in a reaction containing ChemR23 and TIG2 polypeptides without the sample to the amount of the activity measured in a reaction containing ChemR23, TIG2 and the sample, wherein a change in the activity in the presence of the sample relative to the activity in the absence of the sample indicates the presence, in the sample, of an agent that modulates the function of ChemR23.

The invention further encompasses a method of detecting the presence, in a sample, of an agent that modulates the function of ChemR23, the method comprising: a) contacting a

ChemR23 polypeptide with the sample; b) measuring a signaling activity of the ChemR23 polypeptide in the presence of the sample; and c) comparing the activity measured in the presence of the sample to the activity measured in a reaction in which the ChemR23 polypeptide is contacted with a TIG2 polypeptide present at its EC_{50}, wherein an agent that modulates the function of ChemR23 is detected if the amount of the activity measured in the presence of the sample is at least 50% of the amount induced by the TIG2 polypeptide present at its EC_{50}.

In a preferred embodiment of each of the preceding methods, the TIG2 polypeptide is detectably labeled. It is preferred that the TIG2 polypeptide is detectably labeled with a moiety selected from the group consisting of a radioisotope, a fluorophore, a quencher of fluorescence, an enzyme, an affinity tag, and an epitope tag.

In one embodiment of any of the preceding methods, the contacting is performed in or on a cell expressing the ChemR23 polypeptide.

In another embodiment of any of the preceding methods, the contacting is performed in or on synthetic liposomes (see Tajib et al., 2000, *Nature Biotechnology* 18: 649 – 654, which is incorporated herein by reference) or virus-induced budding membranes containing a ChemR23 polypeptide. (see WO0102551, 2001, incorporated herein by reference).

In another embodiment of any of the preceding methods, the method is performed using a membrane fraction from cells expressing the ChemR23 polypeptide.

In another embodiment, the agent is selected from the group consisting of a peptide, a polypeptide, an antibody or antigen-binding fragment thereof, a lipid, a carbohydrate, a nucleic acid, and a small organic molecule.

In another embodiment, the step of measuring a signaling activity of the ChemR23 polypeptide comprises detecting a change in the level of a second messenger.

In another embodiment, the step of measuring a signaling activity comprises measurement of guanine nucleotide binding or exchange, adenylate cyclase activity, cAMP, Protein Kinase C activity, phosphatidylinosotol breakdown, diacylglycerol, inositol triphosphate,

intracellular calcium, arachinoid acid, MAP kinase activity, tyrosine kinase activity, or reporter gene expression.

In a preferred embodiment, the measuring a signaling activity comprises using an aequorin-based assay.

The invention further encompasses a method of modulating the activity of a ChemR23 polypeptide in a cell, the method comprising the step of delivering to the cell an agent that modulates the activity of a ChemR23 polypeptide, such that the activity of ChemR23 is modulated.

The invention further encompasses a method of diagnosing a disease or disorder characterized by dysregulation of ChemR23 signaling, the method comprising: a) contacting a tissue sample with an antibody specific for a ChemR23 polypeptide; b) detecting binding of the antibody to the tissue sample; and c) comparing the binding detected in step (b) with a standard, wherein a difference in binding relative to the standard is diagnostic of a disease or disorder characterized by dysregulation of ChemR23.

The invention further encompasses a method of diagnosing a disease or disorder characterized by dysregulation of ChemR23 signaling, the method comprising: a) contacting a tissue sample with an antibody specific for a TIG2 polypeptide; b) detecting binding of the antibody to the tissue sample; and c) comparing the binding detected in step (b) with a standard, wherein a difference in binding relative to the standard is diagnostic of a disease or disorder characterized by dysregulation of ChemR23.

The invention further encompasses a method of diagnosing a disease or disorder characterized by dysregulation of ChemR23 signaling, the method comprising: a) contacting a tissue sample with an antibody specific for a ChemR23 polypeptide and an antibody specific for a TIG2 polypeptide; b) detecting binding of the antibodies to the tissue sample; and c) comparing the binding detected in step (b) with a standard, wherein a difference in the binding of either antibody or both, relative to the standard, is diagnostic of a disease or disorder characterized by dysregulation of ChemR23.

The invention further encompasses a method of diagnosing a disease or disorder characterized by dysregulation of ChemR23 signaling, the method comprising: a) isolating nucleic acid from a tissue sample; b) amplifying a ChemR23 polynucleotide, using the nucleic acid as a template; and c) comparing the amount of amplified ChemR23 polynucleotide produced in step (b) with a standard, wherein a difference in the amount of amplified ChemR23 polynucleotide relative to the standard is diagnostic of a disease or disorder characterized by dysregulation of ChemR23. In a preferred embodiment, the step of amplifying comprises RT/PCR. In another preferred embodiment, the step of comparing the amount is performed on a microarray.

The invention further encompasses a method of diagnosing a disease or disorder characterized by dysregulation of ChemR23 signaling, the method comprising: a) isolating nucleic acid from a tissue sample; b) amplifying a ChemR23 polynucleotide, using the nucleic acid as a template; and c) comparing the sequence of the amplified ChemR23 polynucleotide produced in step (b) with a standard, wherein a difference in the sequence, relative to the standard is diagnostic of a disease or disorder characterized by dysregulation of ChemR23. In a preferred embodiment, the step of amplifying comprises RT/PCR. In another preferred embodiment, the standard is SEQ ID NO: 1. In another preferred embodiment, the step of comparing the sequence comprises minisequencing. In another preferred embodiment, the step of comparing the sequence is performed on a microarray.

The invention further encompasses a method of diagnosing a disease or disorder characterized by dysregulation of ChemR23 signaling, the method comprising: a) isolating nucleic acid from a tissue sample; b) amplifying a TIG2 polynucleotide, using the nucleic acid as a template; and c) comparing the amount of amplified TIG2 polynucleotide produced in step (b) with a standard, wherein a difference in the amount of amplified TIG2 polynucleotide relative to the standard is diagnostic of a disease or disorder characterized by dysregulation of ChemR23. In a preferred embodiment, the step of amplifying comprises RT/PCR. In another preferred embodiment, the step of comparing the amount is performed on a microarray.

The invention further encompasses a method of diagnosing a disease or disorder characterized by dysregulation of ChemR23 signaling, the method comprising: a) isolating nucleic acid from a tissue sample; b) amplifying a TIG2 polynucleotide, using the nucleic acid as a template; and c) comparing the sequence of the amplified TIG2 polynucleotide produced in step (b) with a standard, wherein a difference in the sequence, relative to the standard is diagnostic of a disease or disorder characterized by dysregulation of ChemR23. In a preferred embodiment, the step of amplifying comprises RT/PCR. In another preferred embodiment, the standard is SEQ ID NO: 7. In another preferred embodiment, the step of comparing the sequence comprises minisequencing. In another preferred embodiment, the step of comparing the sequence is performed on a microarray.

The invention further encompasses a composition comprising an isolated ChemR23 polypeptide and an isolated TIG2 polypeptide.

The invention further encompasses an antibody specific for a Chem R23 polypeptide or a TIG2 polypeptide.

The invention further encompasses a kit for screening for agents that modulate ChemR23 signaling, or for the diagnosis of a disease or disorder characterized by dysregulation of a ChemR23 polypeptide, the kit comprising an isolated ChemR23 polypeptide and packaging materials therefor. In a preferred embodiment, the kit further comprises a TIG2 polypeptide. Diagnostic kits according to the invention permit the determination of whether, for example, a tissue sample or an extract prepared from a tissue sample has an elevated level or activity of TIG2 or ChemR23. The kits also permit the identification of mutations in genes encoding ChemR23 or TIG2 and detection of abnormal levels of nucleic acids encoding ChemR23 or TIG2.

The invention further encompasses a kit for screening for agents that modulate ChemR23 signaling, or for the diagnosis of a disease or disorder characterized by dysregulation of a ChemR23 polypeptide, the kit comprising an isolated polynucleotide encoding a ChemR23 polypeptide and packaging materials therefor. In a preferred embodiment, the kit further comprises an isolated polynucleotide encoding a TIG2 polypeptide.

The invention further encompasses a kit for screening for agents that modulate ChemR23 signaling, or for the diagnosis of a disease or disorder characterized by dysregulation of a ChemR23 polypeptide, the kit comprising a cell transformed with a polynucleotide encoding a ChemR23 polypeptide and packaging materials therefor. In a preferred embodiment, the kit further comprises an isolated polynucleotide encoding a TIG2 polypeptide or a cell comprising a polynucleotide encoding a TIG2 polypeptide.

The invention further encompasses a non-human mammal having a homozygous null mutation in the gene encoding ChemR23.

The invention further encompasses a non-human mammal transgenic for a ChemR23 polynucleotide.

The invention further encompasses a non-human mammal transgenic for a TIG2 polynucleotide.

As used herein, the term "ChemR23 polypeptide" refers to a polypeptide having two essential properties: 1) a ChemR23 polypeptide has at least 70% amino acid identity, and preferably 80%, 90%, 95% or higher, including 100% amino acid identity, to SEQ ID NO: 2; and 2) a ChemR23 polypeptide has ChemR23 activity, i.e., the polypeptide binds a TIG2 polypeptide or a functional fragment thereof. Optimally, a "ChemR23 polypeptide" also has ChemR23 signaling activity as defined herein.

As used herein, the term "ChemR23 polynucleotide" refers to a polynucleotide that encodes a ChemR23 polypeptide as defined herein.

As used herein, the term "ChemR23 activity" refers to specific binding of a TIG2 polypeptide or a functional fragment thereof by a ChemR23 polypeptide.

As used herein, the term "ChemR23 signaling activity" refers to the initiation or propagation of signaling by a ChemR23 polypeptide. ChemR23 signaling activity is monitored by measuring a detectable step in a signaling cascade by assaying one or more of the following: stimulation of GDP for GTP exchange on a G protein; alteration of adenylate cyclase activity; protein kinase C modulation; phosphatidylinositol breakdown (generating second messengers

diacylglycerol, and inositol triphosphate); intracellular calcium flux; activation of MAP kinases; modulation of tyrosine kinases; or modulation of gene or reporter gene activity. A detectable step in a signaling cascade is considered initiated or mediated if the measurable activity is altered by 10% or more above or below a baseline established in the substantial absence of a TIG2 polypeptide relative to any of the ChemR23 activity assays described herein below. The measurable activity can be measured directly, as in, for example, measurement of cAMP or diacylglycerol levels. Alternatively, the measurable activity can be measured indirectly, as in, for example, a reporter gene assay.

As used herein, the term "detectable step" refers to a step that can be measured, either directly, e.g., by measurement of a second messenger or detection of a modified (e.g., phosphorylated) protein, or indirectly, e.g., by monitoring a downstream effect of that step. For example, adenylate cyclase activation results in the generation of cAMP. The activity of adenylate cyclase can be measured directly, e.g., by an assay that monitors the production of cAMP in the assay, or indirectly, by measurement of actual levels of cAMP.

As used herein, the term "isolated" refers to a population of molecules, e.g., polypeptides or polynucleotides, the composition of which is less than 50% (by weight), preferably less than 40% and most preferably 2% or less, contaminating molecules of an unlike nature. When the term "isolated" is applied to a ChemR23 polypeptide, it is specifically meant to encompass a ChemR23 polypeptide that is associated with or embedded in a lipid membrane.

As used herein, the term "TIG2 polypeptide" refers to a polypeptide having at least 31% identity (or higher identity, such as 45%, 55%, 65%, 75%, 85%, 95% or even 100%) to the polypeptide represented by SEQ ID NO: 8 that specifically binds to and activates a signaling activity of a ChemR23 polypeptide having the sequence of SEQ ID NO: 2. The term "specifically binds" means that the TIG2 polypeptide has an EC_{50}, IC_{50},or a K_d of 100nM or less. "TIG2 polypeptide" also refers to a fragment of a polypeptide meeting the preceding definition, wherein the fragment retains at least 50% of the binding activity and level of signaling activation of the full length polypeptide of SEQ ID NO:8. A TIG2 polypeptide can comprise additions, insertions, deletions or substitutions relative to SEQ ID NO: 8, as long as the resulting polypeptide retains at least 50% of the binding activity and level of signaling activation of the

full length polypeptide represented by SEQ ID NO: 8. In addition to the sequences necessary for binding to ChemR23 and activating a ChemR23 signaling actitity, a TIG2 polypeptide can comprise additional sequences, as in for example, a TIG2 fusion protein. Non-limiting examples of fusion partners include glutathione-S-transferase (GST), maltose binding protein, alkaline phosphatase, thioredoxin, green fluorescent protein (GFP), histidine tags (e.g., 6X or greater His), or epitope tags (e.g., Myc tag, FLAG tag).

As used herein, the term "TIG2 polynucleotide" refers to a polynucleotide that encodes a TIG2 polypeptide as defined herein, or the complement thereof.

As used herein, the terms "candidate compound" and "candidate modulator" refer to a composition being evaluated for the ability to modulate ligand binding to a ChemR23 polypeptide or the ability to modulate an activity of a ChemR23 polypeptide. Candidate modulators can be natural or synthetic compounds, including, for example, small molecules, compounds contained in extracts of animal, plant, bacterial or fungal cells, as well as conditioned medium from such cells.

As used herein, the term "small molecule" refers to a compound having molecular mass of less than 3000 Daltons, preferably less than 2000 or 1500, still more preferably less than 1000, and most preferably less than 600 Daltons. A "small organic molecule" is a small molecule that comprises carbon.

As used herein, the term "change in binding" or "change in activity" and the equivalent terms "difference in binding" or "difference in activity" refer to an at least 10% increase or decrease in binding, or signaling activity in a given assay.

As used herein, the term "conditions permitting the binding of TIG2 to ChemR23" refers to conditions of, for example, temperature, salt concentration, pH and protein concentration under which TIG2 binds ChemR23. Exact binding conditions will vary depending upon the nature of the assay, for example, whether the assay uses viable cells or only membrane fraction of cells. However, because ChemR23 is a cell surface protein, and because TIG2 is a secreted polypeptide that interacts with ChemR23 on the cell surface, favored conditions will generally include physiological salt (90 mM) and pH (about 7.0 to 8.0). Temperatures for binding can

vary from 15°C to 37°C, but will preferably be between room temperature and about 30°C. The concentration of TIG2 and ChemR23 polypeptide in a binding reaction will also vary, but will preferably be about 0.1 pM(e.g., in a reaction with radiolabeled tracer TIG2, where the concentration is generally below the K_d) to 1 μM (e.g., TIG2 as competitor). As an example, for a binding assay using ChemR23-expressing cells and purified, recombinant, labeled TIG2 polypeptide, binding is performed using 0.1 nM labeled TIG2, 100 nM cold TIG2, and 25,000 cells at 27°C in 250 μl of a binding buffer consisting of 50 mM HEPES (pH 7.4), 1 mM $CaCl_2$, and 0.5% Fatty acid free BSA.

As used herein, the term "sample" refers to the source of molecules being tested for the presence of an agent that modulates binding to or signaling activity of a ChemR23 polypeptide. A sample can be an environmental sample, a natural extract of animal, plant yeast or bacterial cells or tissues, a clinical sample, a synthetic sample, or a conditioned medium from recombinant cells or a fermentation processe. The term "tissue sample" refers to a tissue that is tested for the presence, abundance, quality or an activity of a ChemR23 polypeptide, a TIG2 polypeptide, a nucleic acid encoding a ChemR23 or TIG2 polypeptide, or an agent that modifies the ligand binding or activity of a ChemR23 polypeptide.

As used herein, a "tissue" is an aggregate of cells that perform a particular function in an organism. The term "tissue" as used herein refers to cellular material from a particular physiological region. The cells in a particular tissue can comprise several different cell types. A non-limiting example of this would be brain tissue that further comprises neurons and glial cells, as well as capillary endothelial cells and blood cells, all contained in a given tissue section or sample. In addition to solid tissues, the term "tissue" is also intended to encompass non-solid tissues, such as blood.

As used herein, the term "membrane fraction" refers to a preparation of cellular lipid membranes comprising a ChemR23 polypeptide. As the term is used herein, a "membrane fraction" is distinct from a cellular homogenate, in that at least a portion (i.e., at least 10%, and preferably more) of non-membrane-associated cellular constituents has been removed. The term "membrane associated" refers to those cellular constituents that are either integrated into a lipid

membrane or are physically associated with a component that is integrated into a lipid membrane.

As used herein, the term "decrease in binding" refers to a decrease of at least 10% in the binding of a TIG2 polypeptide or other agonist to a ChemR23 polypeptide as measured in a binding assay as described herein.

As used herein, the term "second messenger" refers to a molecule, generated or caused to vary in concentration by the activation of a G-Protein Coupled Receptor, that participates in the transduction of a signal from that GPCR. Non-limiting examples of second messengers include cAMP, diacylglycerol, inositol triphosphates and intracellular calcium. The term "change in the level of a second messenger" refers to an increase or decrease of at least 10% in the detected level of a given second messenger relative to the amount detected in an assay performed in the absence of a candidate modulator.

As used herein, the term "aequorin-based assay" refers to an assay for GPCr activity that measures intracellular calcium flux induced by activated GPCRs, wherein intracellular calcium flux is measured by the luminescence of aequorin expressed in the cell.

As used herein, the term "binding" refers to the physical association of a ligand (e.g., a TIG2 polypeptide) with a receptor (e.g., ChemR23). As the term is used herein, binding is "specific" if it occurs with an EC_{50} or a K_d of 100 nM or less, generally in the range of 100 nM to 10 pM. For example, binding is specific if the EC_{50} or K_d is 100nM, 50nM, 10 nM, 1 nM, 950 pM, 900 pM, 850 pM, 800 pM, 750 pM, 700 pM, 650 pM, 600 pM, 550 pM, 500 pM, 450 pM, 400 pM, 350 pM, 300 pM, 250 pM, 200 pM, 150 pM, 100 pM, 75 pM, 50 pM, 25 pM or 10 pM or less.

As used herein, the term "EC_{50}," refers to that concentration of an agent at which a given activity, including binding of a TIG2 polypeptide or other ligand and a functional activity of a ChemR23 polypeptide, is 50% of the maximum for that ChemR23 activity measurable using the same assay. Stated differently, the "EC_{50}" is the concentration of agent that gives 50% activation, when 100% activation is set at the amount of activity that does not increase with the addition of more agonist. It should be noted that the "EC_{50} of a TIG2 polypeptide" will vary

with the identity of the TIG2 polypeptide; for example, variant TIG2 polypeptides (i.e., those containing insertions, deletions, substitutions or fusions with other polypeptides, including TIG2 molecules from species other than humans and variants of them that satisfy the definition of TIG2 polypeptide set forth above) can have EC_{50} values higher than, lower than or the same as wild-type TIG2. Therefore, where a TIG2 variant sequence differs from wild-type TIG2 of SEQ ID NO:8, one of the skill in the art can determine the EC_{50} for that variant according to conventional methods. The EC_{50} of a given TIG2 polypeptide is measured by performing an assay for an activity of a fixed amount of ChemR23 polypeptide in the presence of doses of the TIG2 polypeptide that increase at least until the ChemR23 response is saturated or maximal, and then plotting the measured ChemR23 activity versus the concentration of TIG2 polypeptide.

As used herein, the term "IC_{50}" is the concentration of an antagonist or inverse agonist that reduces the maximal activation of a ChemR23 receptor by 50%.

As used herein, the term "detectably labeled" refers to the property of a molecule, e.g., a TIG2 polypeptide or other ChemR23 ligand, that has a structural modification that incorporates a functional group (label) that can be readily detected. Detectable labels include but are not limited to fluorescent compounds, isotopic compounds, chemiluminescent compounds, quantum dot labels, biotin, enzymes, electron-dense reagents, and haptens or proteins for which antisera or monoclonal antibodies are available. The various means of detection include but are not limited to spectroscopic, photochemical, radiochemical, biochemical, immunochemical, or chemical means.

As used herein, the term "affinity tag" refers to a label, attached to a molecule of interest (e.g., a TIG2 polypeptide or other ChemR23 ligand), that confers upon the labeled molecule the ability to be specifically bound by a reagent that binds the label. Affinity tags include, but are not limited to an epitope for an antibody (known as "epitope tags"), biotin, 6X His, and GST. Affinity tags can be used for the detection, as well as for the purification of the labeled species.

As used herein, the term "decrease in binding" refers to a decrease of at least 10% in the amount of binding detected in a given assay with a known or suspected modulator of ChemR23 relative to binding detected in an assay lacking that known or suspected modulator.

As used herein, the term "delivering," when used in reference to a drug or agent, means the addition of the drug or agent to an assay mixture, or to a cell in culture. The term also refers to the administration of the drug or agent to an animal. Such administration can be, for example, by injection (in a suitable carrier, e.g., sterile saline or water) or by inhalation, or by an oral, transdermal, rectal, vaginal, or other common route of drug administration.

As used herein, the term "effective amount" refers to that amount of a drug or ChemR23 modulating agent that results in a change in a ChemR23 activity as defined herein (i.e., at least 10% increase or decrease in a ChemR23 activity).

As used herein, the term "standard" refers to a sample taken from an individual who is not affected by a disease or disorder characterized by dysregulation of ChemR23 or TIG2 activity. The "standard" is used as a reference for the comparison of ChemR23 or TIG2 polypeptide or mRNA levels and quality (i.e., mutant vs. wild-type), as well as for the comparison of ChemR23 activities.

As used herein, the term "amplifying," when applied to a nucleic acid sequence, refers to a process whereby one or more copies of a nucleic acid sequence is generated from a template nucleic acid. A preferred method of "amplifying" is PCR or RT/PCR.

As used herein, the term "substantial absence" refers to a level of an activating or inhibiting factor that is below the level necessary to activate or inhibit GPCR function by at least 10% as measured by a given assay disclosed herein or known in the art.

As used herein, the term "G-Protein coupled receptor," or "GPCR" refers to a membrane-associated polypeptide with 7 alpha helical transmembrane domains. Functional GPCR's associate with a ligand or agonist and also associate with and activate G-proteins. ChemR23 is a GPCR.

As used herein, the term "agent that modulates the function of a ChemR23 polypeptide" is a molecule or compound that increases or decreases ChemR23 activity, including compounds that change the binding of TIG2 polypeptides or other agonists, and compounds that change ChemR23 downstream signaling activities.

As used herein, the term "transgenic animal" refers to any animal, preferably a non-human mammal, bird, fish or an amphibian, in which one or more of the cells of the animal contain heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or *in vitro* fertilization, but rather is directed to the introduction of a recombinant DNA molecule. This molecule may be integrated within a chromosome, or it may be extra-chromosomally replicating DNA. In the typical transgenic animals described herein, the transgene causes cells to express a recombinant form of one of the subject polypeptide, e.g. either agonistic or antagonistic forms. However, transgenic animals in which the recombinant gene is silent are also contemplated, as for example, the FLP or CRE recombinase dependent constructs described below. Moreover, "transgenic animal" also includes those recombinant animals in which gene disruption of one or more genes is caused by human intervention, including both recombination and antisense techniques.

As used herein, the term "antibody" is the conventional immunoglobulin molecule, as well as fragments thereof which are also specifically reactive with one of the subject polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described herein below for whole antibodies. For example, $F(ab)_2$ fragments can be generated by treating antibody with pepsin. The resulting $F(ab)_2$ fragment can be treated to reduce disulfide bridges to produce Fab fragments. The antibody of the present invention is further intended to include bispecific, single-chain, and chimeric and humanized molecules having affinity for a polypeptide conferred by at least one CDR region of the antibody. In preferred embodiments, the antibodies, the antibody further comprises a label attached thereto and able to be detected, (e.g., the label can be a radioisotope, fluorescent compound, chemiluminescent compound, enzyme, or enzyme co-factor).

As used herein, the term "null mutation" refers to an insertion, deletion, or substitution that modifies the chromosomal sequences encoding a polypeptide, such that the polypeptide is not expressed.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows the nucleotide (SEQ ID NO: 1) and deduced amino acid sequence of human ChemR23/Dezb/CMKRL1.

Figure 2 shows the amino acid sequence of human ChemR23/Dezb/CMKRL1 (SEQ ID NO: 2). The seven predicted transmembrane domains are underlined. The consensus sequence for N-linked glycosylation (N-X-S/T) in the N terminus is bold, and the potential site of phosphorylation by PKC (S/T-X-R/K) in the C terminus is italicized.

Figure 3 shows the nucleotide (SEQ ID NO:3) and deduced amino acid (SEQ ID NO: 4) sequences of mouse Dez, the mouse orthologue of ChemR23.

Figure 4 shows that nucleotide (SEQ ID NO: 5) and deduced amino acid (SEQ ID NO: 6) sequences of rat G-Protein –Coupled Chemoattractant-1, the rat orthologue of ChemR23/Dezb/ CMKRL1.

Figure 5 shows the structural similarities between the amino acid sequences of ChemR23/ Dezb/CMKRL1and the sequences of AT2, C3a, c5a, and fMLP receptors and selected chemokine receptor sequences performed using the ClustalX algorithm. The dendrogram shown was constructed using the TreeView Algorithm.

Figure 6 shows the nucleotide (SEQ ID NO: 7) and deduced amino acid (SEQ ID NO: 8) sequences of human TIG2.

Figure 7 shows the nucleotide (SEQ ID NO: 9) and deduced amino acid (SEQ ID NO: 10) sequences of mouse TIG2.

Figure 8 shows an alignment of the human and mouse TIG2 amino acid sequences. Identical amino acids are conservatove substitutions are boxed.

Figure 9 shows an alignment of human, mouse, rat, sus, bos, and Gallus gallus TIG2 sequences. The figure provides the percent amino acid identity across any two species listed.

Figure 10 shows a partial chromatogram of the fifth step of purification of TIG2 from ascitic fluid. The active fractions (eluted with approximately 28% CH_3CN) of the previous step were diluted 6 fold with 0.1% TFA in H_2O and directly loaded onto a C18 reverse phase column (1mm x 50 mm, Vydac) pre-equilabrated with 5% CH_3CN/0.1% TFA in H_2O at a flow-rate of 0.1 ml/min. at room temperature. A 5-95% gradient of CH_3CN in 0.1%TFA was applied with a 0.3%/min slope between 25 and 45%. The activity was eluted at 40% CH_3CN (indicated by the black horizontal line).

Figure 11 shows the identification of a specific response for Chemr23 following screening of HPLC fractions obtained from the fractionation of human ovary ascites. The different fractions obtained following fractionation of human ovary ascites were diluted fivefold in the assay buffer and tested in an aequorin assay using a cell line expressing ChemR23 (open circles) or cell lines expressing unrelated receptors (closed triangles and squares). The response obtained for each fraction was normalized using the ATP response of each cell line.

Figure 12 shows the activation of ChemR23 by conditioned medium of 293T cells transiently transfected with TIG2. 293T cells were transiently transfected with pCDNA3-TIG2 or with pCDNA3 alone (mock transfected). Increasing volumes of the supernatant collected 4 days after transfection were analyzed using a Microlumat in an aequorin-based assay with CHO cells expressing ChemR23. The assay was performed in triplicate, and SD is indicated. A representative experiment is shown.

Figure 13 shows the characterization of antibodies directed against ChemR23 by flow cytometry.

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to the discovery that TIG2 polypeptide is a natural ligand for the orphan ChemR23 GPCR. The interaction is useful for screening assays for agents that modulate the interaction and thus the function of ChemR23. The known ligand and its interaction with the receptor also provides for the diagnosis of conditions involving dysregulated receptor activity.

I. Assays For The Identification Of Agents That Modulate The Activity Of ChemR23

Agents that modulate the activity of ChemR23 can be identified in a number of ways that take advantage of the interaction of the receptor with TIG2. For example, the ability to reconstitute ChemR23/TIG2 binding either in vitro, on cultured cells or in vivo provides a target for the identification of agents that disrupt that binding. Assays based on disruption of binding can identify agents, such as small organic molecules, from libraries or collections of such molecules. Alternatively, such assays can identify agents in samples or extracts from natural sources, e.g., plant, fungal or bacterial extracts or even in human tissue samples (e.g., tumor tissue). In one aspect, the extracts can be made from cells expressing a library of variant nucleic acids, peptides or polypeptides, including, for example, variants of TIG2 polypeptide itself. Modulators of ChemR23/TIG2 binding can then be screened using a binding assay or a functional assay that measures downstream signaling through the receptor. Both binding assays and functional assays are validated using TIG2 polypeptide.

Another approach that uses the ChemR23/TIG2 interaction more directly to identify agents that modulate ChemR23 function measures changes in ChemR23 downstream signaling induced by candidate agents or candidate modulators. These functional assays can be performed in isolated cell membrane fractions or on cells expressing the receptor on their surfaces.

The following description provides methods for both binding and functional assays based upon the interaction of ChemR23 and TIG2.

A. ChemR23 polypeptides.

Assays using the interaction of ChemR23 and TIG2 require a source of ChemR23 polypeptide. The polynucleotide and polypeptide sequence of human ChemR23 are presented herein as SEQ ID NOs: 1 and 2. The human ChemR23 polynucleotide sequence is also available at GenBank Accession No. Y14838, and was reported in Samson et al., 1998, Eur. J. Immunol. 28: 1689-1700, incorporated herein by reference. ChemR23 polypeptide sequence is also recorded at accession Nos. O75748 and CAA75112 in the Swissprot database. Related sequences include those for CMKRL1 (GenBank Accession Nos. XM_006864 and NM004072 (nucleotide sequences) and Swissprot Accession No. Q99788 (polypeptide sequence)), human DEZb (GenBank Accession No. U79527 (nucleotide sequence)), human DEZa (GenBank Accession No. U79526 (nucleotide sequence), mouse DEZ (GenBank Accession No. U79525

(nucleotide sequence) and Swissprot Accession No. P97468 (polypeptide sequence)), and rat ChemR23 (GenBank Accession No. AJ002745 (nucleotide sequence) and Swissprot Accession No. 035786 (polypeptide sequence).

One skilled in the art can readily amplify a ChemR23 sequence from a sample containing mRNA encoding the protein through basic PCR and molecular cloning techniques using primers or probes designed from the known sequences.

The expression of recombinant polypeptides is well known in the art. Those skilled in the art can readily select vectors and expression control sequences for the expression of ChemR23 polypeptides useful according to the invention in eukaryotic or prokaryotic cells. ChemR23 must be associated with cell membrane or detergents like synthetic liosomes in order to have binding or signaling function. Methods for the preparation of cellular membrane fractions are well known in the art, e.g., the method reported by Hubbard & Cohn, 1975, J. Cell Biol. 64: 461-479, which is incorporated herein by reference. In order to produce membranes comprising ChemR23, one need only apply such techniques to cells endogenously or recombinantly expressing ChemR23. Alternatively, membrane-free ChemR23 can be integrated into membrane preparations by dilution of detergent solution of the polypeptide (see, e.g., Salamon et al., 1996, Biophys. J. 71:283-294, which is incorporated herein by reference).

B. TIG2 polypeptides.

Human TIG2 polynucleotide and polypeptide sequences are presented herein as SEQ ID Nos 7 and 8, respectively. TIG2 sequences are also available from GenBank (e.g., Human polynucleotide sequences include Accession Nos. XM 004765, U77594, NM 002889, human polypeptide sequence is available at Accession Nos. Q99969, BAA76499, AAB47975, NP002880, and XP004765; Gallus gallus polynucleotide sequences include Accession Nos. BG713704, BG713660 and BG713614; mouse polynucleotide sequences include BF020273, AW113641 and bf018000; rat polynucleotide sequences include AW915104; Sus scrofa polynucleotide sequences include BF078978 and BF713092 (overlapping ESTs, last 7 amino acids of TIG2 sequence in BF713092); and Bos taurus polynucleotide sequences include BG691132). An alignment of TIG2 sequences is presented in Figure 9.

As with ChemR23, TIG2 polynucleotides can be cloned through standard PCR and molecular cloning techniques using the known sequences as a source of amplification primers or probes. Similarly, cloned TIG2 polypeptides can be expressed in eukaryotic or prokaryotic cells as known in the art. As a non-limiting example, a mammalian TIG2 expression vector system can comprise a bicistronic expression vector containing the promoter of human EF1α (described by Mishizuma & Nagata, 1990, Nucl. Acids Res. 18: 5322), a polylinker, the ECMV internal ribosome entry site (IRES, described by Ghattas et al., 1991, Mol. Cell. Biol. 11: 5848-5859) and the neomycin resistance gene followed by an SV40 polyA signal. A TIG2 expression construct for expression in yeast is described in Example 4.

TIG2 can also be expressed in vitro through in vitro transcription and translation. Further, if desired for a given assay or technique, TIG2 polypeptides useful according to the invention can be produced as fusion proteins or tagged proteins. For example, either full length TIG2 or a portion thereof (i.e., at least 10 amino acids, preferably at least 20 amino acids or more, up to one amino acid less than full length TIG2) can be fused to Glutathione-S-Transferase (GST), secreted alkaline phosphatase (SEAP), a FLAG tag, a Myc tag, or a 6X-His peptide to facilitate the purification or detection of the TIG2 polypeptide. Methods and vectors for the production of tagged or fusion proteins are well known in the art, as are methods of isolating and detecting such fused or tagged proteins.

Recombinant TIG2 polypeptides can be used in purified form. Alternatively, conditioned medium from TIG2 transfected cells can be used. The amounts of TIG2 necessary in a given binding or functional assay according to the invention will vary depending upon the assay, but will generally use 1 pM to 1 nM of labeled and 10 pM to 1μM of unlabeled TIG2 per assay. The affinities and EC_{50}s of tagged TIG2 polypeptides for ChemR23 may vary relative to those of full length wild type TIG2 polypeptide, and the amount necessary for a given assay can therefore be adjusted relative to the wild-type values. If necessary for a given assay, TIG2 can be labeled by incorporation of radiolabeled amino acids in the medium during synthesis, e.g., ^{35}S-Met, ^{14}C-Leu, or others as appropriate. Methods of chemical labeling with ^{125}I are known in the art. Fluorescent labels can also be attached to TIG2 polypeptides or to other ChemR23 ligands using standard labeling techniques.

C. Assays to Identify Modulators of ChemR23 Activity

The discovery that TIG2 is a ligand of the ChemR23 receptor permits screening assays to identify agonists, antagonists and inverse agonists of receptor activity. The screening assays will have two general approaches.

1) Ligand binding assays, in which cells expressing ChemR23, membrane extracts from such cells, or immobilized lipid membranes comprising ChemR23 are exposed to a labeled TIG2 polypeptide and candidate compound. Following incubation, the reaction mixture is measured for specific binding of the labeled TIG2 polypeptide to the ChemR23 receptor. Compounds that interfere with or displace labeled TIG2 polypeptide can be agonists, antagonists or inverse agonists of ChemR23 activity. Functional analysis can be performed on positive compounds to determine which of these categories they fit.

2) Functional assays, in which a signaling activity of ChemR23 is measured.

a) For agonist screening, cells expressing ChemR23 or membranes prepared from them are incubated with candidate compound, and a signaling activity of ChemR23 is measured. The assays are validated using a TIG2 polypeptide as agonist, and the activity induced by compounds that modulate receptor activity is compared to that induced by TIG2. An agonist or partial agonist will have a maximal biological activity corresponding to at least 10% of the maximal activity of wild type human TIG2 when the agonist or partial agonist is present at 10 μM or less, and preferably will have 50%, 75%, 100% or more, including 2-fold, 5-fold, 10-fold or more activity than wild-type human TIG2.

b) For antagonist or inverse agonist screening, cells expressing ChemR23 or membranes isolated from them are assayed for signaling activity in the presence of a TIG2 polypeptide with or without a candidate compound. Antagonists or inverse agonists will reduce the level of TIG2-stimulated receptor activity by at least 10%, relative to reactions lacking the antagonist or inverse agonist.

c) For inverse agonist screening, cells expressing constitutive ChemR23 activity or membranes isolated from them are used in a functional assay that measures an activity of the receptor in the presence and absence of a candidate compound. Inverse agonists are those

compounds that reduce the constitutive activity of the receptor by at least 10%. Overexpression of ChemR23 (i.e., expression of 5-fold or higher excess of ChemR23 polypeptide relative to the level naturally expressed in macro phages in vivo) may lead to constitutive activation. Chem R23 can be overexpressed by placing it under the control of a strong constitutive promoter, e.g., the CMV early promoter. Alternatively, certain mutations of conserved GPCR amino acids or amino acid domains tend to lead to constitutive activity. See for example: Kjelsberg et al., 1992, J. Biol. Chem. 267:1430; McWhinney et al., 2000. J. Biol. Chem. 275:2087; Ren et al., 1993, J. Biol. Chem. 268:16483; Samama et al., 1993, J.Biol.Chem 268:4625; Parma et al., 1993, Nature 365:649; Parma et al., 1998, J. Pharmacol. Exp. Ther. 286:85; and Parent et al., 1996, J. Biol. Chem. 271:7949.

Ligand binding and displacement assays:

One can use ChemR23 polypeptides expressed on a cell, or isolated membranes containing receptor polypeptides, along with a TIG2 polypeptide in order to screen for compounds that inhibit the binding of TIG2 to ChemR23. When identified in an assay that measures binding or TIG2 polypeptide displacement alone, compounds will have to be subjected to functional testing to determine whether they act as agonists, antagonists or inverse agonists.

For displacement experiments, cells expressing a ChemR23 polypeptide (generally 25,000 cells per assay or 1 to 100 μg of membrane extracts) are incubated in binding buffer (e.g., 50 mM Hepes pH 7.4; 1 mM $CaCl_2$; 0.5% Bovine Serum Albumin (BSA) Fatty Acid-Free; and 0 5 mM $MgCl_2$) for 1.5 hrs (at, for example, 27°C) with labeled TIG2 polypeptide in the presence or absence of increasing concentrations of a candidate modulator. To validate and calibrate the assay, control competition reactions using increasing concentrations of unlabeled TIG2 polypeptide can be performed. After incubation, cells are washed extensively, and bound, labeled TIG2 is measured as appropriate for the given label (e.g., scintillation counting, enzyme assay, fluorescence, etc.). A decrease of at least 10% in the amount of labeled TIG2 polypeptide bound in the presence of candidate modulator indicates displacement of binding by the candidate modulator. Candidate modulators are considered to bind specifically in this or other assays described herein if they displace 50% of labeled TIG2 (sub-saturating TIG2 dose) at a concentration of 10 μM or less (i.e., EC_{50} is 10 μM or less).

Alternatively, binding or displacement of binding can be monitored by surface plasmon resonance (SPR). Surface plasmon resonance assays can be used as a quantitative method to measure binding between two molecules by the change in mass near an immobilized sensor caused by the binding or loss of binding of a TIG2 polypeptide from the aqueous phase to a ChemR23 polypeptide immobilized in a membrane on the sensor. This change in mass is measured as resonance units versus time after injection or removal of the TIG2 polypeptide or candidate modulator and is measured using a Biacore Biosensor (Biacore AB). ChemR23 can be immobilized on a sensor chip (for example, research grade CM5 chip; Biacore AB) in a thin film lipid membrane according to methods described by Salamon et al. (Salamon et al., 1996, Biophys J. 71: 283-294; Salamon et al., 2001, Biophys. J. 80: 1557-1567; Salamon et al., 1999, Trends Biochem. Sci. 24: 213-219, each of which is incorporated herein by reference.). Sarrio et al. demonstrated that SPR can be used to detect ligand binding to the GPCR A(1) adenosine receptor immobilized in a lipid layer on the chip (Sarrio et al., 2000, Mol. Cell. Biol. 20: 5164-5174, incorporated herein by reference). Conditions for TIG2 binding to ChemR23 in an SPR assay can be fine-tuned by one of skill in the art using the conditions reported by Sarrio et al. as a starting point.

SPR can assay for modulators of binding in at least two ways. First, a TIG2 polypeptide can be pre-bound to immobilized ChemR23 polypeptide, followed by injection of candidate modulator at approximately 10 µl/min flow rate and a concentration ranging from 1 nM to 100 µM, preferably about 1 µM. Displacement of the bound TIG2 can be quantitated, permitting detection of modulator binding. Alternatively, the membrane-bound ChemR23 polypeptide can be pre-incubated with candidate modulator and challenged with a TIG2 polypeptide. A difference in TIG2 binding to the ChemR23 exposed to modulator relative to that on a chip not pre-exposed to modulator will demonstrate binding. In either assay, a decrease of 10% or more in the amount of a TIG2 polypeptide bound is in the presence of candidate modulator, relative to the amount of a TIG2 polypeptide bound in the absence of candidate modulator indicates that the candidate modulator inhibits the interaction of ChemR23 and TIG2.

Another method of measuring inhibition of binding of a TIG2 polypeptide to ChemR23 uses fluorescence resonance energy transfer (FRET). FRET is a quantum mechanical

phenomenon that occurs between a fluorescence donor (D) and a fluorescence acceptor (A) in close proximity to each other (usually < 100 A of separation) if the emission spectrum of D overlaps with the excitation spectrum of A. The molecules to be tested, e.g., a TIG2 polypeptide and a ChemR23 polypeptide, are labeled with a complementary pair of donor and acceptor fluorophores. While bound closely together by the ChemR23:TIG2 interaction, the fluorescence emitted upon excitation of the donor fluorophore will have a different wavelength than that emitted in response to that excitation wavelength when the polypeptides are not bound, providing for quantitation of bound versus unbound polypeptides by measurement of emission intensity at each wavelength. Donor:Acceptor pairs of fluorophores with which to label the polypeptides are well known in the art. Of particular interest are variants of the *A. victoria* GFP known as Cyan FP (CFP, Donor(D)) and Yellow FP (YFP, Acceptor(A)). The GFP variants can be made as fusion proteins with the respective members of the binding pair to serve as D-A pairs in a FRET scheme to measure protein-protein interaction. Vectors for the expression of GFP variants as fusions are known in the art. As an example, a CFP-TIG2 fusion and a YFP-ChemR23 fusion can be made. The addition of a candidate modulator to the mixture of labeled TIG2 and ChemR23 proteins will result in an inhibition of energy transfer evidenced by, for example, a decrease in YFP fluorescence relative to a sample without the candidate modulator. In an assay using FRET for the detection of ChemR23:TIG2 interaction, a 10% or greater decrease in the intensity of fluorescent emission at the acceptor wavelength in samples containing a candidate modulator, relative to samples without the candidate modulator, indicates that the candidate modulator inhibits ChemR23:TIG2 interaction.

A variation on FRET uses fluorescence quenching to monitor molecular interactions. One molecule in the interacting pair can be labeled with a fluorophore, and the other with a molecule that quenches the fluorescence of the fluorophore when brought into close apposition with it. A change in fluorescence upon excitation is indicative of a change in the association of the molecules tagged with the fluorophore:quencher pair. Generally, an increase in fluorescence of the labeled ChemR23 polypeptide is indicative that the TIG2 polypeptide bearing the quencher has been displaced. For quenching assays, a 10% or greater increase in the intensity of fluorescent emission in samples containing a candidate modulator, relative to samples without the candidate modulator, indicates that the candidate modulator inhibits ChemR23:TIG2 interaction.

In addition to the surface plasmon resonance and FRET methods, fluorescence polarization measurement is useful to quantitate protein-protein binding. The fluorescence polarization value for a fluorescently-tagged molecule depends on the rotational correlation time or tumbling rate. Protein complexes, such as those formed by ChemR23 associating with a fluorescently labeled TIG2 polypeptide, have higher polarization values than uncomplexed, labeled TIG2. The inclusion of a candidate inhibitor of the ChemR23:TIG2 interaction results in a decrease in fluorescence polarization, relative to a mixture without the candidate inhibitor, if the candidate inhibitor disrupts or inhibits the interaction of ChemR23 with TIG2. Fluorescence polarization is well suited for the identification of small molecules that disrupt the formation of polypeptide or protein complexes. A decrease of 10% or more in fluorescence polarization in samples containing a candidate modulator, relative to fluorescence polarization in a sample lacking the candidate modulator, indicates that the candidate modulator inhibits ChemR23:TIG2 interaction.

Another alternative for monitoring ChemR23:TIG2 interactions uses a biosensor assay. ICS biosensors have been described by AMBRI (Australian Membrane Biotechnology Research Institute; http//www.ambri.com.au/). In this technology, the association of macromolecules such as ChemR23 and TIG2, is coupled to the closing of gramacidin-facilitated ion channels in suspended membrane bilayers and thus to a measurable change in the admittance (similar to impedence) of the biosensor. This approach is linear over six orders of magnitude of admittance change and is ideally suited for large scale, high throughput screening of small molecule combinatorial libraries. A 10% or greater change (increase or decrease) in admittance in a sample containing a candidate modulator, relative to the admittance of a sample lacking the candidate modulator, indicates that the candidate modulator inhibits the interaction of ChemR23 and TIG2.

It is important to note that in assays of protein-protein interaction, it is possible that a modulator of the interaction need not necessarily interact directly with the domain(s) of the proteins that physically interact. It is also possible that a modulator will interact at a location removed from the site of protein-protein interaction and cause, for example, a conformational change in the ChemR23 polypeptide. Modulators (inhibitors or agonists) that act in this manner are nonetheless of interest as agents to modulate the activity of ChemR23.

It should be understood that any of the binding assays described herein can be performed with a non-TIG2 ligand (for example, agonist, antagonist, etc.) of ChemR23, e.g., a small molecule identified as described herein. In practice, the use of a small molecule ligand or other non-TIG2 ligand has the benefit that non-polypeptide chemical compounds are generally cheaper and easier to produce in purified form than polypeptides such as TIG2. Thus, a non-TIG2 ligand is better suited to high-throughput assays for the identification of agonists, antagonists or inverse agonists than full length TIG2. This advantage in no way erodes the importance of assays using TIG2, however, as such assays are well suited for the initial identification of non-TIG2 ligands.

Any of the binding assays described can be used to determine the presence of an agent in a sample, e.g., a tissue sample, that binds to the ChemR23 receptor molecule, or that affects the binding of TIG2 to the receptor. To do so, ChemR23 polypeptide is reacted with TIG2 polypeptide or another ligand in the presence or absence of the sample, and TIG2 or ligand binding is measured as appropriate for the binding assay being used. A decrease of 10% or more in the binding of TIG2 or other ligand indicates that the sample contains an agent that modulates TIG2 or ligand binding to the receptor polypeptide.

Functional assays of receptor activity

i. GTPase/GTP Binding Assays:

For GPCRs such as ChemR23, a measure of receptor activity is the binding of GTP by cell membranes containing receptors. In the method described by Traynor and Nahorski, 1995, Mol. Pharmacol. 47: 848-854, incorporated herein by reference, one essentially measures G-protein coupling to membranes by measuring the binding of labeled GTP. For GTP binding assays, membranes isolated from cells expressing the receptor are incubated in a buffer containing 20 mM HEPES, pH 7.4, 100 mM NaCl, and 10 mM MgCl2, 80 pM ^{35}S-GTPγS and 3 μM GDP. The assay mixture is incubated for 60 minutes at 30°C, after which unbound labeled GTP is removed by filtration onto GF/B filters. Bound, labeled GTP is measured by liquid scintillation counting. In order to assay for modulation of TIG2-induced ChemR23 activity, membranes prepared from cells expressing a ChemR23 polypeptide are mixed with a TIG2 polypeptide, and the GTP binding assay is performed in the presence and absence of a candidate modulator of ChemR23 activity. A decrease of 10% or more in labeled GTP binding as

measured by scintillation counting in an assay of this kind containing candidate modulator, relative to an assay without the modulator, indicates that the candidate modulator inhibits ChemR23 activity.

A similar GTP-binding assay can be performed without TIG2 to identify compounds that act as agonists. In this case, TIG2-stimulated GTP binding is used as a standard. A compound is considered an agonist if it induces at least 50% of the level of GTP binding induced by full length wild-type TIG2 when the compound is present at 1 μM or less, and preferably will induce a level the same as or higher than that induced by TIG2.

GTPase activity is measured by incubating the membranes containing a ChemR23 polypeptide with γ^{32}P-GTP. Active GTPase will release the label as inorganic phosphate, which is detected by separation of free inorganic phosphate in a 5% suspension of activated charcoal in 20 mM H_3PO_4, followed by scintillation counting. Controls include assays using membranes isolated from cells not expressing ChemR23 (mock-transfected), in order to exclude possible non-specific effects of the candidate compound.

In order to assay for the effect of a candidate modulator on ChemR23-regulated GTPase activity, membrane samples are incubated with a TIG2 polypeptide, with and without the modulator, followed by the GTPase assay. A change (increase or decrease) of 10% or more in the level of GTP binding or GTPase activity relative to samples without modulator is indicative of ChemR23 modulation by a candidate modulator.

ii. Downstream Pathway Activation Assays:

a. Calcium flux - The Aequorin-based Assay.

The aequorin assay takes advantage of the responsiveness of mitochondrial apoaequorin to intracellular calcium release induced by the activation of GPCRs (Stables et al., 1997, Anal. Biochem. 252:115-126; Detheux et al., 2000, J. Exp. Med., 192 1501-1508; both of which are incorporated herein by reference). Briefly, ChemR23-expressing clones are transfected to coexpress mitochondrial apoaequorin and Gα16. Cells are incubated with 5 μM Coelenterazine H (Molecular Probes) for 4 hours at room temperature, washed in DMEM-F12 culture medium and resuspended at a concentration of 0.5 x 10^6 cells/ml. Cells are then mixed with test agonist

peptides and light emission by the aequorin is recorded with a luminometer for 30 sec. Results are expressed as Relative Light Units (RLU). Controls include assays using membranes isolated from cells not expressing ChemR23 (mock-transfected), in order to exclude possible non-specific effects of the candidate compound.

Aequorin activity or intracellular calcium levels are "changed" if light intensity increases or decreases by 10% or more in a sample of cells, expressing a ChemR23 polypeptide and treated with a candidate modulator, relative to a sample of cells expressing the ChemR23 polypeptide but not treated with the candidate modulator or relative to a sample of cells not expressing the ChemR23 polypeptide (mock-transfected cells) but treated with the candidate modulator.

When performed in the absence of a TIG2 polypeptide, the assay can be used to identify an agonist of ChemR23 activity. When the assay is performed in the presence of a TIG2 polypeptide, it can be used to assay for an antagonist.

b. Adenylate Cyclase Assay:

Assays for adenylate cyclase activity are described by Kenimer & Nirenberg, 1981, Mol. Pharmacol. 20: 585-591, incorporated herein by reference. That assay is a modification of the assay taught by Solomon et al., 1974, Anal. Biochem. 58: 541-548, also incorporated herein by reference. Briefly, 100 µl reactions contain 50 mM Tris-Hcl (pH 7.5), 5 mM $MgCl_2$, 20 mM creatine phosphate (disodium salt), 10 units (71 µg of protein) of creatine phosphokinase, 1 mM α-^{32}P-ATP (tetrasodium salt, 2 µCi), 0.5 mM cyclic AMP, G-^{3}H-labeled cyclic AMP (approximately 10,000 cpm), 0.5 mM Ro20-1724, 0.25% ethanol, and 50-200 µg of protein homogenate to be tested (i.e., homogenate from cells expressing or not expressing a ChemR23 polypeptide, treated or not treated with a TIG2 polypeptide with or without a candidate modualtor). Reaction mixtures are generally incubated at 37°C for 6 minutes. Following incubation, reaction mixtures are deproteinized by the addition of 0.9 ml of cold 6% trichloroacetic acid. Tubes are centrifuged at 1800 x g for 20 minutes and each supernatant solution is added to a Dowex AG50W-X4 column. The cAMP fraction from the column is eluted with 4 ml of 0.1 mM imidazole-HCl (pH 7.5) into a counting vial. Assays should be

performed in triplicate. Control reactions should also be performed using protein homogenate from cells that do not express a ChemR23 polypeptide.

According to the invention, adenylate cyclase activity is "changed" if it increases or decreases by 10% or more in a sample taken from cells treated with a candidate modulator of ChemR23 activity, relative to a similar sample of cells not treated with the candidate modulator or relative to a sample of cells not expressing the ChemR23 polypeptide (mock-transfected cells) but treated with the candidate modulator.

c. cAMP Assay:

Intracellular or extracellular cAMP is measured using a cAMP radioimmunoassay (RIA) or cAMP binding protein according to methods widely known in the art. For example, Horton & Baxendale, 1995, Methods Mol. Biol. 41: 91-105, which is incorporated herein by reference, describes an RIA for cAMP.

A number of kits for the measurement of cAMP are commercially available, such as the High Efficiency Fluorescence Polarization-based homogeneous assay marketed by LJL Biosystems and NEN Life Science Products. Control reactions should be performed using extracts of mock-transfected cells to exclude possible non-specific effects of some candidate modulators.

The level of cAMP is "changed" if the level of cAMP detected in cells, expressing a ChemR23 polypeptide and treated with a candidate modulator of ChemR23 activity (or in extracts of such cells), using the RIA-based assay of Horton & Baxendale, 1995, supra, increases or decreases by at least 10% relative to the cAMP level in similar cells not treated with the candidate modulator.

d. Phospholipid breakdown, DAG production and Inositol Triphosphate levels:

Receptors that activate the breakdown of phospholipids can be monitored for changes due to the activity of known or suspected modulators of ChemR23 by monitoring phospholipid breakdown, and the resulting production of second messengers DAG and/or inositol triphosphate (IP_3). Methods of measuring each of these are described in Phospholipid Signaling Protocols, edited by Ian M. Bird. Totowa, NJ, Humana Press, 1998, which is incorporated herein by

reference. See also Rudolph et al., 1999, J. Biol. Chem. 274: 11824-11831, incorporated herein by reference, which also describes an assay for phosphatidylinositol breakdown. Assays should be performed using cells or extracts of cells expressing ChemR23, treated or not treated with a TIG2 polypeptide with or without a candidate modulator. Control reactions should be performed using mock-transfected cells, or extracts from them in order to exclude possible non-specific effects of some candidate modulators.

According to the invention, phosphatidylinositol breakdown, and diacylglycerol and/or inositol triphosphate levels are "changed" if they increase or decrease by at least 10% in a sample from cells expressing a ChemR23 polypeptide and treated with a candidate modulator, relative to the level observed in a sample from cells expressing a ChemR23 polypeptide that is not treated with the candidate modulator.

e. PKC activation assays:

Growth factor receptor tyrosine kinases tend to signal via a pathway involving activation of Protein Kinase C (PKC), which is a family of phospholipid- and calcium-activated protein kinases. PKC activation ultimately results in the transcription of an array of proto-oncogene transcription factor-encoding genes, including c-fos, c-myc and c-jun, proteases, protease inhibitors, including collagenase type I and plasminogen activator inhibitor, and adhesion molecules, including intracellular adhesion molecule I (ICAM I). Assays designed to detect increases in gene products induced by PKC can be used to monitor PKC activation and thereby receptor activity. In addition, the activity of receptors that signal via PKC can be monitored through the use of reporter gene constructs driven by the control sequences of genes activated by PKC activation. This type of reporter gene-based assay is discussed in more detail below.

For a more direct measure of PKC activity, the method of Kikkawa et al., 1982, J. Biol. Chem. 257: 13341, incorporated herein by reference, can be used. This assay measures phosphorylation of a PKC substrate peptide, which is subsequently separated by binding to phosphocellulose paper. This PKC assay system can be used to measure activity of purified kinase, or the activity in crude cellular extracts. Protein kinase C sample can be diluted in 20 mM HEPES/ 2 mM DTT immediately prior to assay.

The substrate for the assay is the peptide Ac-FKKSFKL-NH2, derived from the myristoylated alanine-rich protein kinase C substrate protein (MARCKS). The K_m of the enzyme for this peptide is approximately 50 μM. Other basic, protein kinase C-selective peptides known in the art can also be used, at a concentration of at least 2 -3 times their K_m. Cofactors required for the assay include calcium, magnesium, ATP, phosphatidylserine and diacylglycerol. Depending upon the intent of the user, the assay can be performed to determine the amount of PKC present (activating conditions) or the amount of active PCK present (non-activating conditions). For most purposes according to the invention, non-activating conditions will be used, such that the PKC that is active in the sample when it is isolated is measured, rather than measuring the PKC that can be activated. For non-activating conditions, calcium is omitted in the assay in favor of EGTA.

The assay is performed in a mixture containing 20 mM HEPES, pH 7.4, 1-2 mM DTT, 5 mM $MgCl_2$, 100 μM ATP, ~1 μCi γ-^{32}P-ATP, 100 μg/ml peptide substrate (~100 μM), 140 μM / 3.8 μM phosphatidylserine/diacylglycerol membranes, and 100 μM calcium (or 500 μM EGTA). 48 μl of sample, diluted in 20 mM HEPES, pH 7.4, 2 mM DTT is used in a final reaction volume of 80 μl. Reactions are performed at 30°C for 5-10 minutes, followed by addition of 25 μl of 100 mM ATP, 100 mM EDTA, pH 8.0, which stops the reactions.

After the reaction is stopped, a portion (85 μl) of each reaction is spotted onto a Whatman P81 cellulose phosphate filter, followed by washes: four times 500 ml in 0.4% phosphoric acid, (5-10 min per wash); and a final wash in 500 ml 95% EtOH, for 2-5 min. Bound radioactivity is measured by scintillation counting. Specific activity (cpm/nmol) of the labeled ATP is determined by spotting a sample of the reaction onto P81 paper and counting without washing. Units of PKC activity, defined as nmol phosphate transferred per min, are calculated as follows:

The activity, in UNITS (nmol/min) is:

$$= \frac{\text{(cpm on paper) x (105 μl total /85 μl spotted)}}{\text{(assay time, min) (specific activity of ATP cpm/nmol).}}$$

An alternative assay can be performed using a Protein Kinase C Assay Kit sold by PanVera (Cat. # P2747).

Assays are performed on extracts from cells expressing a ChemR23 polypeptide, treated or not treated with a TIG2 polypeptide with or without a candidate modulator. Control reactions should be performed using mock-transfected cells, or extracts from them in order to exclude possible non-specific effects of some candidate modulators.

According to the invention, PKC activity is "changed" by a candidate modulator when the units of PKC measured by either assay described above increase or decrease by at least 10%, in extracts from cells expressing ChemR23 and treated with a candidate modulator, relative to a reaction performed on a similar sample from cells not treated with a candidate modulator.

f. Kinase assays:

MAP kinase activity can be assayed using any of several kits available commercially, for example, the p38 MAP Kinase assay kit sold by New England Biolabs (Cat # 9820) or the FlashPlate™ MAP Kinase assays sold by Perkin-Elmer Life Sciences.

MAP Kinase activity is "changed" if the level of activity is increased or decreased by 10% or more in a sample from cells, expressing a ChemR23 polypeptide, treated with a candidate modulator relative to MAP kinase activity in a sample from similar cells not treated with the candidate modulator.

Direct assays for tyrosine kinase activity using known synthetic or natural tyrosine kinase substrates and labeled phosphate are well known, as are similar assays for other types of kinases (e.g., Ser/Thr kinases). Kinase assays can be performed with both purified kinases and crude extracts prepared from cells expressing a ChemR23 polypeptide, treated with or without a TIG2 polypeptide, with or without a candidate modulator. Control reactions should be performed using mock-transfected cells, or extracts from them in order to exclude possible non-specific effects of some candidate modulators. Substrates can be either full length protein or synthetic peptides representing the substrate. Pinna & Ruzzene (1996, Biochem. Biophys. Acta 1314: 191-225, incorporated herein by reference) list a number of phosphorylation substrate sites useful for measuring kinase activities. A number of kinase substrate peptides are commercially available. One that is particularly useful is the "Src-related peptide," RRLIEDAEYAARG (SEQ

ID NO: 11; available from Sigma # A7433), which is a substrate for many receptor and nonreceptor tyrosine kinases. Because the assay described below requires binding of peptide substrates to filters, the peptide substrates should have a net positive charge to facilitate binding. Generally, peptide substrates should have at least 2 basic residues and a free amino terminus. Reactions generally use a peptide concentration of 0.7-1.5 mM.

Assays are generally carried out in a 25 µl volume comprising 5 µl of 5X kinase buffer (5 mg/mL BSA, 150 mM Tris-Cl (pH 7.5), 100 mM $MgCl_2$; depending upon the exact kinase assayed for, $MnCl_2$ can be used in place of or in addition to the $MgCl_2$), 5 µl of 1.0 mM ATP (0.2 mM final concentration), γ-32P-ATP (100-500 cpm/pmol), 3 µl of 10 mM peptide substrate (1.2 mM final concentration), cell extract containing kinase to be tested (cell extracts used for kinase assays should contain a phosphatase inhibitor (e.g. 0.1-1 mM sodium orthovanadate)), and H_2O to 25 µl. Reactions are performed at 30°C, and are initiated by the addition of the cell extract.

Kinase reactions are performed for 30 seconds to about 30 minutes, followed by the addition of 45µl of ice-cold 10% trichloroacetic acid (TCA). Samples are spun for 2 minutes in a microcentrifuge, and 35µl of the supernatant is spotted onto Whatman P81 cellulose phosphate filter circles. The filters are washed three times with 500 ml cold 0.5% phosphoric acid, followed by one wash with 200 ml of acetone at room temperature for 5 minutes. Filters are dried and incorporated 32P is measured by scintillation counting. The specific activity of ATP in the kinase reaction (e.g., in cpm/pmol) is determined by spotting a small sample (2-5 µl) of the reaction onto a P81 filter circle and counting directly, without washing. Counts per minute obtained in the kinase reaction (minus blank) are then divided by the specific activity to determine the moles of phosphate transferred in the reaction.

Tyrosine kinase activity is "changed" if the level of kinase activity is increased or decreased by 10% or more in a sample from cells, expressing a ChemR23 polypeptide, treated with a candidate modulator relative to kinase activity in a sample from similar cells not treated with the candidate modulator.

g. Transcriptional reporters for downstream pathway activation:

The intracellular signal initiated by binding of an agonist to a receptor, e.g., ChemR23, sets in motion a cascade of intracellular events, the ultimate consequence of which is a rapid and detectable change in the transcription or translation of one or more genes. The activity of the receptor can therefore be monitored by measuring the expression of a reporter gene driven by control sequences responsive to ChemR23 activation.

As used herein "promoter" refers to the transcriptional control elements necessary for receptor-mediated regulation of gene expression, including not only the basal promoter, but also any enhancers or transcription-factor binding sites necessary for receptor-regulated expression. By selecting promoters that are responsive to the intracellular signals resulting from agonist binding, and operatively linking the selected promoters to reporter genes whose transcription, translation or ultimate activity is readily detectable and measurable, the transcription based reporter assay provides a rapid indication of whether a given receptor is activated.

Reporter genes such as luciferase, CAT, GFP, β-lactamase or β-galactosidase are well known in the art, as are assays for the detection of their products.

Genes particularly well suited for monitoring receptor activity are the "immediate early" genes, which are rapidly induced, generally within minutes of contact between the receptor and the effector protein or ligand. The induction of immediate early gene transcription does not require the synthesis of new regulatory proteins. In addition to rapid responsiveness to ligand binding, characteristics of preferred genes useful to make reporter constructs include: low or undetectable expression in quiescent cells; induction that is transient and independent of new protein synthesis; subsequent shut-off of transcription requires new protein synthesis; and mRNAs transcribed from these genes have a short half-life. It is preferred, but not necessary that a transcriptional control element have all of these properties for it to be useful.

An example of a gene that is responsive to a number of different stimuli is the c-fos proto-oncogene. The c-fos gene is activated in a protein-synthesis-independent manner by growth factors, hormones, differentiation-specific agents, stress, and other known inducers of cell surface proteins. The induction of c-fos expression is extremely rapid, often occurring within minutes of receptor stimulation. This characteristic makes the c-fos regulatory regions particularly attractive for use as a reporter of receptor activation.

The c-fos regulatory elements include (see, Verma et al., 1987, Cell 51: 513-514): a TATA box that is required for transcription initiation; two upstream elements for basal transcription, and an enhancer, which includes an element with dyad symmetry and which is required for induction by TPA, serum, EGF, and PMA.

The 20 bp c-fos transcriptional enhancer element located between -317 and -298 bp upstream from the c-fos mRNA cap site, is essential for serum induction in serum starved NIH 3T3 cells. One of the two upstream elements is located at –63 to -57 and it resembles the consensus sequence for cAMP regulation.

The transcription factor CREB (cyclic AMP responsive element binding protein) is, as the name implies, responsive to levels of intracellular cAMP. Therefore, the activation of a receptor that signals via modulation of cAMP levels can be monitored by measuring either the binding of the transcription factor, or the expression of a reporter gene linked to a CREB-binding element (termed the CRE, or cAMP response element). The DNA sequence of the CRE is TGACGTCA (SEQ ID NO: 12). Reporter constructs responsive to CREB binding activity are described in U.S. Patent No. 5,919,649.

Other promoters and transcriptional control elements, in addition to the c-fos elements and CREB-responsive constructs, include the vasoactive intestinal peptide (VIP) gene promoter (cAMP responsive; Fink et al., 1988, Proc. Natl. Acad. Sci. 85:6662-6666); the somatostatin gene promoter (cAMP responsive; Montminy et al., 1986, Proc. Natl. Acad. Sci. 8.3:6682-6686); the proenkephalin promoter (responsive to cAMP, nicotinic agonists, and phorbol esters; Comb et al., 1986, Nature 323:353-356); the phosphoenolpyruvate carboxy-kinase (PEPCK) gene promoter (cAMP responsive; Short et al., 1986, J. Biol. Chem. 261:9721-9726).

Additional examples of transcriptional control elements that are responsive to changes in GPCR activity include, but are not limited to those responsive to the AP-1 transcription factor and those responsive to NF-κB activity. The consensus AP-1 binding site is the palindrome TGA(C/G)TCA (Lee et al., 1987, *Nature* 325: 368-372; Lee et al., 1987, *Cell* 49: 741-752). The AP-1 site is also responsible for mediating induction by tumor promoters such as the phorbol ester 12-*O*-tetradecanoylphorbol-β-acetate (TPA), and are therefore sometimes also referred to as a TRE, for TPA-response element. AP-1 activates numerous genes that are involved in the

early response of cells to growth stimuli. Examples of AP-1-responsive genes include, but are not limited to the genes for Fos and Jun (which proteins themselves make up AP-1 activity), Fos-related antigens (Fra) 1 and 2, IκBα, ornithine decarboxylase, and annexins I and II.

The NF-κB binding element has the consensus sequence GGGGACTTTCC. A large number of genes have been identified as NF-κB responsive, and their control elements can be linked to a reporter gene to monitor GPCR activity. A small sample of the genes responsive to NF-κB includes those encoding IL-1β (Hiscott et al., 1993, Mol. Cell. Biol. 13: 6231-6240), TNF-α (Shakhov et al., 1990, J. Exp. Med. 171: 35-47), CCR5 (Liu et al., 1998, AIDS Res. Hum. Retroviruses 14: 1509-1519), P-selectin (Pan & McEver, 1995, J. Biol. Chem. 270: 23077-23083), Fas ligand (Matsui et al., 1998, J. Immunol. 161: 3469-3473), GM-CSF (Schreck & Baeuerle, 1990, Mol. Cell. Biol. 10: 1281-1286) and IκBα (Haskill et al., 1991, Cell 65: 1281-1289). Each of these references is incorporated herein by reference. Vectors encoding NF-κB-responsive reporters are also known in the art or can be readily made by one of skill in the art using, for example, synthetic NF-κB elements and a minimal promoter, or using the NF-κB-responsive sequences of a gene known to be subject to NF-κB regulation. Further, NF-κB responsive reporter constructs are commercially available from, for example, CLONTECH.

A given promoter construct should be tested by exposing ChemR23-expressing cells, transfected with the construct, to a TIG2 polypeptide. An increase of at least two-fold in the expression of reporter in response to TIG2 polypeptide indicates that the reporter is an indicator of ChemR23 activity.

In order to assay ChemR23 activity with a TIG2-responsive transcriptional reporter construct, cells that stably express a ChemR23 polypeptide are stably transfected with the reporter construct. To screen for agonists, the cells are left untreated, exposed to candidate modulators, or exposed to a a TIG2 polypeptide, and expression of the reporter is measured. The TIG2-treated cultures serve as a standard for the level of transcription induced by a known agonist. An increase of at least 50% in reporter expression in the presence of a candidate modulator indicates that the candidate is a modulator of ChemR23 activity. An agonist will induce at least as much, and preferably the same amount or more, reporter expression than the TIG2 polypeptide. This approach can also be used to screen for inverse agonists where cells

express a ChemR23 polypeptide at levels such that there is an elevated basal activity of the reporter in the absence of TIG2 or another agonist. A decrease in reporter activity of 10% or more in the presence of a candidate modulator, relative to its absence, indicates that the compound is an inverse agonist.

To screen for antagonists, the cells expressing ChemR23 and carrying the reporter construct are exposed to a TIG2 polypeptide (or another agonist) in the presence and absence of candidate modulator. A decrease of 10% or more in reporter expression in the presence of candidate modulator, relative to the absence of the candidate modulator, indicates that the candidate is a modulator of ChemR23 activity.

Controls for transcription assays include cells not expressing ChemR23 but carrying the reporter construct, as well as cells with a promoterless reporter construct. Compounds that are identified as modulators of ChemR23-regulated transcription should also be analyzed to determine whether they affect transcription driven by other regulatory sequences and by other receptors, in order to determine the specificity and spectrum of their activity.

The transcriptional reporter assay, and most cell-based assays, are well suited for screening expression libraries for proteins for those that modulate ChemR23 activity. The libraries can be, for example, cDNA libraries from natural sources, e.g., plants, animals, bacteria, etc., or they can be libraries expressing randomly or systematically mutated variants of one or more polypeptides. Genomic libraries in viral vectors can also be used to express the mRNA content of one cell or tissue, in the different libraries used for screening of ChemR23.

Any of the assays of receptor activity, including the GTP-binding, GTPase, adenylate cyclase, cAMP, phospholipid-breakdown, diacylglyceorl, inositol triphosphate, PKC, kinase and transcriptional reporter assays, can be used to determine the presence of an agent in a sample, e.g., a tissue sample, that affects the activity of the ChemR23 receptor molecule. To do so, ChemR23 polypeptide is assayed for activity in the presence and absence of the sample or an extract of the sample. An increase in ChemR23 activity in the presence of the sample or extract relative to the absence of the sample indicates that the sample contains an agonist of the receptor activity. A decrease in receptor activity in the presence of TIG2 or another agonist and the sample, relative to receptor activity in the presence of TIG2 polypeptide alone, indicates that the

sample contains an antagonist of ChemR23 activity. If desired, samples can then be fractionated and further tested to isolate or purify the agonist or antagonist. The amount of increase or decrease in measured activity necessary for a sample to be said to contain a modulator depends upon the type of assay used. Generally, a 10% or greater change (increase or decrease) relative to an assay performed in the absence of a sample indicates the presence of a modulator in the sample. One exception is the transcriptional reporter assay, in which at least a two-fold increase or 10% decrease in signal is necessary for a sample to be said to contain a modulator. It is preferred that an agonist stimulates at least 50%, and preferably 75% or 100% or more, e.g., 2-fold, 5-fold, 10-fold or greater receptor activation than wild-type TIG2.

Other functional assays include, for example, microphysiometer or biosensor assays (see Hafner, 2000, *Biosens. Bioelectron.* 15: 149-158, incorporated herein by reference).

II. Diagnostic Assays Based upon the Interaction of ChemR23 and TIG2:

Signaling through GPCRs is instrumental in the pathology of a large number of diseases and disorders. ChemR23, which is expressed in cells of the lymphocyte lineages and which has been shown to act as a co-receptor for immunodeficiency viruses can have a role in immune processes, disorders or diseases. The ChemR23 expression pattern also includes bone and cartilage, indicating that this receptor can play a role in diseases, disorders or processes (e.g., fracture healing) affecting these tissues. Expression in adult parathyroid suggests possible importance in phosphocalic metabolism.

Because of its expression in cells of the lymphocyte lineages, ChemR23 can be involved in the body's response to viral infections or in diseases induced by various viruses, including HIV types I and II, or bacteria. The expression pattern of ChemR23 and the knowledge with respect to disorders generally mediated by GPCRs suggests that ChemR23 can be involved in disturbances of cell migration, cancer, development of tumours and tumour metastasis, inflammatory and neo-plastic processes, wound and bone healing and dysfunction of regulatory growth functions, diabetes, obesity, anorexia, bulimia, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, restenosis, atherosclerosis, diseases characterised by excessive smooth muscle cell proliferation, aneurysms, diseases characterised by loss of smooth muscle cells or reduced smooth muscle cell

proliferation, stroke, ischemia, ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, depression, delirium, dementia and severe mental retardation, degenerative diseases, neurodegenerative diseases such as Alzheimer's disease or Parkinson's disease, and dyskinasias, such as Huntington's disease or Gilles de la Tourett's syndrome and other related diseases.

The interaction of ChemR23 with TIG2 can be used as the basis of assays for the diagnosis or monitoring of diseases, disorders or processes involving ChemR23 signaling. Diagnostic assays for ChemR23-related diseases or disorders can have several different forms. First, diagnostic assays can measure the amount of ChemR23 and/or TIG2 polypeptide, genes or mRNA in a sample of tissue. Assays that measure the amount of mRNA encoding either or both of these polypeptides also fit in this category. Second, assays can evaluate the qualities of the receptor or the ligand. For example, assays that determine whether an individual expresses a mutant or variant form of either ChemR23 or TIG2, or both, can be used diagnostically. Third, assays that measure one or more activities of ChemR23 polypeptide can be used diagnostically.

A. Assays that measure the amount of ChemR23 or TIG2

ChemR23 and TIG2 levels can be measured and compared to standards in order to determine whether an abnormal level of the receptor or its ligand is present in a sample, either of which indicate probable dysregulation of ChemR23 signaling. Polypeptide levels are measured, for example, by immunohistochemistry using antibodies specific for the polypeptide. A sample isolated from an individual suspected of suffering from a disease or disorder characterized by ChemR23 activity is contacted with an antibody for ChemR23 or TIG2, and binding of the antibody is measured as known in the art (e.g., by measurement of the activity of an enzyme conjugated to a secondary antibody).

Another approach to the measurement of ChemR23 and/or TIG2 polypeptide levels uses flow cytometry analysis of cells from an affected tissue. Methods of flow cytometry, including the fluorescent labeling of antibodies specific for ChemR23 or TIG2, are well known in the art. Other approaches include radioimmunoassay or ELISA. Methods for each of these are also well known in the art.

The amount of binding detected is compared to the binding in a sample of similar tissue from a healthy individual, or from a site on the affected individual that is not so affected. An increase of 10% or more relative to the standard is diagnostic for a disease or disorder characterized by ChemR23 dysregulation.

ChemR23 and TIG2 expression can also be measured by determining the amount of mRNA encoding either or both of the polypeptides in a sample of tissue. mRNA can be quantitated by quantitative or semi-quantitative PCR. Methods of "quantitative" amplification are well known to those of skill in the art, and primer sequences for the amplification of both ChemR23 and TIG2 are disclosed herein. A common method of quantitative PCR involves simultaneously co-amplifying a known quantity of a control sequence using the same primers. This provides an internal standard that can be used to calibrate the PCR reaction. Detailed protocols for quantitative PCR are provided in PCR Protocols, A Guide to Methods and Applications, Innis et al., Academic Press, Inc. N.Y., (1990), which is incorporated herein by reference. An increase of 10% or more in the amount of mRNA encoding ChemR23 or TIG2 in a sample, relative to the amount expressed in a sample of like tissue from a healthy individual or in a sample of tissue from an unaffected location in an affected individual is diagnostic for a disease or disorder characterized by dysregulation of ChemR23 signaling.

B. Qualitative assays

Assays that evaluate whether or not the ChemR23 polypeptide or the mRNA encoding it are wild-type or not can be used diagnostically. In order to diagnose a disease or disorder characterized by ChemR23 or TIG2 dysregulation in this manner, RNA isolated from a sample is used as a template for PCR amplification of TIG2 and/or ChemR23. The amplified sequences are then either directly sequenced using standard methods, or are first cloned into a vector, followed by sequencing. A difference in the sequence that changes one or more encoded amino acids relative to the sequence of wild-type ChemR23 or TIG2 can be diagnostic of a disease or disorder characterized by dysregulation of ChemR23 signaling. It can be useful, when a change in coding sequence is identified in a sample, to express the variant receptor or ligand and compare its activity to that of wild type ChemR23 or TIG2. Among other benefits, this approach can provide novel mutants, including constitutively active and null mutants.

In addition to standard sequencing methods, amplified sequences can be assayed for the presence of specific mutations using, for example, hybridization of molecular beacons that discriminate between wild-type and variant sequences. Hybridization assays that discriminate on the basis of changes as small as one nucleotide are well known in the art. Alternatively, any of a number of "minisequencing" assays can be performed, including, those described, for example, in U.S. Patents 5,888,819, 6,004,744 and 6,013,431 (incorporated herein by reference). These assays and others known in the art can determine the presence, in a given sample, of a nucleic acid with a known polymorphism.

If desired, array or microarray-based methods can be used to analyze the expression or the presence of mutation, in ChemR23 or TIG2 sequences. Array-based methods for minisequencing and for quantitation of nucleic acid expression are well known in the art.

C. Functional assays.

Diagnosis of a disease or disorder characterized by the dysregulation of ChemR23 signaling can also be performed using functional assays. To do so, cell membranes or cell extracts prepared from a tissue sample are used in an assay of ChemR23 activity as described herein (e.g., ligand binding assays, the GTP-binding assay, GTPase assay, adenylate cyclase assay, cAMP assay, phospholipid breakdown, diacyl glycerol or inositol triphosphate assays, PKC activation assay, or kinase assay). The activity detected is compared to that in a standard sample taken from a healthy individual or from an unaffected site on the affected individual. As an alternative, a sample or extract of a sample can be applied to cells expressing ChemR23, followed by measurement of ChemR23 signaling activity relative to a standard sample. A difference of 10% or more in the activity measured in any of these assays, relative to the activity of the standard, is diagnostic for a disease or disorder characterized by dysregulation of ChemR23 signaling.

Modulation of ChemR23 Activity in a Cell According to the Invention

The discovery of TIG2 as a ligand of ChemR23 provides methods of modulating the activity of a ChemR23 polypeptide in a cell. ChemR23 activity is modulated in a cell by delivering to that cell an agent that modulates the function of a ChemR23 polypeptide. This

modulation can be performed in cultured cells as part of an assay for the identification of additional modulating agents, or, for example, in an animal, including a human. Agents include TIG2 polypeptides as defined herein, as well as additional modulators identified using the screening methods described herein.

An agent can be delivered to a cell by adding it to culture medium. The amount to deliver will vary with the identity of the agent and with the purpose for which it is delivered. For example, in a culture assay to identify antagonists of ChemR23 activity, one will preferably add an amount of TIG2 polypeptide that half-maximally activates the receptors (e.g., approximately EC_{50}), preferably without exceeding the dose required for receptor saturation. This dose can be determined by titrating the amount of TIG2 polypeptide to determine the point at which further addition of TIG2 has no additional effect on ChemR23 activity.

When a modulator of ChemR23 activity is administered to an animal for the treatment of a disease or disorder, the amount administered can be adjusted by one of skill in the art on the basis of the desired outcome. Successful treatment is achieved when one or more measurable aspects of the pathology (e.g., tumor cell growth, accumulation of inflammatory cells) is changed by at least 10% relative to the value for that aspect prior to treatment.

Candidate Modulators Useful According to the Invention

Candidate modulators can be screened from large libraries of synthetic or natural compounds. Numerous means are currently used for random and directed synthesis of saccharide, peptide, lipid, carbohydrate, and nucleic acid based compounds. Synthetic compound libraries are commercially available from a number of companies including, for example, Maybridge Chemical Co. (Trevillet, Cornwall, UK), Comgenex (Princeton, NJ), Brandon Associates (Merrimack, NH), and Microsource (New Milford, CT). A rare chemical library is available from Aldrich (Milwaukee, WI). Combinatorial libraries of small organic molecules are available and can be prepared. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available from e.g., Pan Laboratories (Bothell, WA) or MycoSearch (NC), or are readily produceable by methods well known in the art. Additionally, natural and synthetically produced libraries and compounds are readily modified through conventional chemical, physical, and biochemical means.

As noted previously herein, candidate modulators can also be variants of known polypeptides (e.g., TIG2, antibodies) or nucleic acids (e.g., aptamers) encoded in a nucleic acid library. Cells (e.g., bacteria, yeast or higher eukaryotic cells) transformed with the library can be grown and prepared as extracts, which are then applied in ChemR23 binding assays or functional assays of ChemR23 activity.

Antibodies Useful According to the Invention

The invention provides for antibodies to ChemR23 and TIG2. Antibodies can be made using standard protocols known in the art (See, for example, Antibodies: A Laboratory Manual ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal, such as a mouse, hamster, or rabbit can be immunized with an immunogenic form of the peptide (e.g., a ChemR23 or TIG2 polypeptide or an antigenic fragment which is capable of eliciting an antibody response, or a fusion protein as described herein above). Immunogens for raising antibodies are prepared by mixing the polypeptides (e.g., isolated recombinant polypeptides or synthetic peptides) with adjuvants. Alternatively, ChemR23 or TIG2 polypeptides or peptides are made as fusion proteins to larger immunogenic proteins. Polypeptides can also be covalently linked to other larger immunogenic proteins, such as keyhole limpet hemocyanin. Alternatively, plasmid or viral vectors encoding ChemR23 or TIG2, or a fragment of these proteins, can be used to express the polypeptides and generate an immune response in an animal as described in Costagliola et al., 2000, J. Clin. Invest. 105:803-811, which is incorporated herein by reference. In order to raise antibodies, immunogens are typically administered intradermally, subcutaneously, or intramuscularly to experimental animals such as rabbits, sheep, and mice. In addition to the antibodies discussed above, genetically engineered antibody derivatives can be made, such as single chain antibodies.

The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA, flow cytometry or other immunoassays can also be used with the immunogen as antigen to assess the levels of antibodies. Antibody preparations can be simply serum from an immunized animal, or if desired, polyclonal antibodies can be isolated from the serum by, for example, affinity chromatography using immobilized immunogen.

To produce monoclonal antibodies, antibody-producing splenocytes can be harvested from an immunized animal and fused by standard somatic cell fusion procedures with immortalizing cells such as myeloma cells to yield hybridoma cells. Such techniques are well known in the art, and include, for example, the hybridoma technique (originally developed by Kohler and Milstein, (1975) Nature, 256: 495-497), the human B cell hybridoma technique (Kozbar *et al.,* (1983) Immunology Today, 4: 72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., (1985) Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. pp. 77-96). Hybridoma cells can be screened immunochemically for production of antibodies specifically reactive with a TIG2 or ChemR23 peptide or polypeptide, and monoclonal antibodies isolated from the media of a culture comprising such hybridoma cells.

Transgenic Animals Useful According to the Invention

Transgenic animals expressing ChemR23 or TIG2 or variants thereof are useful to study the signaling through ChemR23, as well as for the study of drugs or agents that modulate the activity of ChemR23. A transgenic animal is a non-human animal containing at least one foreign gene, called a transgene, which is part of its genetic material. Preferably, the transgene is contained in the animal's germ line such that it can be transmitted to the animal's offspring. A number of techniques may be used to introduce the transgene into an animal's genetic material, including, but not limited to, microinjection of the transgene into pronuclei of fertilized eggs and manipulation of embryonic stem cells (U.S. Patent No. 4,873,191 by Wagner and Hoppe; Palmiter and Brinster, 1986, *Ann. Rev. Genet.*, 20:465-499; French Patent Application 2593827 published Aug. 7, 1987, all of which are incorporated herein by reference). Transgenic animals can carry the transgene in all their cells or can be genetically mosaic.

According to the method of conventional transgenesis, additional copies of normal or modified genes are injected into the male pronucleus of the zygote and become integrated into the genomic DNA of the recipient mouse. The transgene is transmitted in a Mendelian manner in established transgenic strains. Transgenes can be constitutively expressed or can be tissue specific or even responsive to an exogenous drug, e.g., Tetracycline. A transgenic animal

expressing one transgene can be crossed to a second transgenic animal expressing a second transgene such that their offspring will carry and express both transgenes.

Knock-Out Animals

Animals bearing a homozygous deletion in the chromosomal sequences encoding either ChemR23 or TIG2 or variants can be used to study the function of the receptor and ligand. Of particular interest is whether a TIG2 knockout has a distinct phenotype, which may point to whether TIG2 is the only ligand that binds ChemR23 or if it is a member of a family. Of further particular interest is the identification of identification of ChemR23/TIG2 in specific physiological and/or pathological processes.

i. Standard knock out animals

Knock out animals are produced by the method of creating gene deletions with homologous recombination. This technique is based on the development of embryonic stem (ES) cells that are derived from embryos, are maintained in culture and have the capacity to participate in the development of every tissue in the animals when introduced into a host blastocyst. A knock out animal is produced by directing homologous recombination to a specific target gene in the ES cells, thereby producing a null allele of the gene. The technology for making knock-out animals is well described (see, for example, Huszar et al., 1997, *Cell*, 88:131; and Ohki-Hamazaki et al., 1997, *Nature*, 390:165, both of which are incorporated herein by reference). One of skill in the art can generate a homozygous ChemR23 or TIG2 knock-out animal (e.g., a mouse) using the sequences for ChemR23 and TIG2 (disclosed herein and known in the art) to make the gene targeting construct.

ii. Tissue specific knock out

The method of targeted homologous recombination has been improved by the development of a system for site-specific recombination based on the bacteriophage P1 site specific recombinase Cre. The Cre-loxP site-specific DNA recombinase from bacteriophage P1 is used in transgenic mouse assays in order to create gene knockouts restricted to defined tissues or developmental stages. Regionally restricted genetic deletion, as opposed to global gene knockout, has the advantage that a phenotype can be attributed to a particular cell/tissue (Marth,

1996, *Clin. Invest.* 97: 1999). In the Cre-loxP system one transgenic mouse strain is engineered such that loxP sites flank one or more exons of the gene of interest. Homozygotes for this so called 'floxed gene' are crossed with a second transgenic mouse that expresses the Cre gene under control of a cell/tissue type transcriptional promoter. Cre protein then excises DNA between loxP recognition sequences and effectively removes target gene function (Sauer, 1998, *Methods*, 14:381). There are now many in vivo examples of this method, including, for instance, the inducible inactivation of mammary tissue specific genes (Wagner et al., 1997, *Nucleic Acids Res.*, 25:4323). One of skill in the art can therefore generate a tissue-specific knock-out animal in which ChemR23 or TIG2 is homozygously eliminated in a chosen tissue or cell type.

Kits Useful According to the Invention

The invention provides for kits useful for screening for modulators of ChemR23 activity, as well as kits useful for diagnosis of diseases or disorders characterized by dysregulation of ChemR23 signaling. Kits useful according to the invention can include an isolated ChemR23 polypeptide (including a membrane-or cell-associated ChemR23 polypeptide, e.g., on isolated membranes, cells expressing ChemR23, or, on an SPR chip) and an isolated TIG2 polypeptide. A kit can also comprise an antibody specific for ChemR23 and/or an antibody for TIG2. Alternatively, or in addition, a kit can contain cells transformed to express a ChemR23 polypeptide and/or cells transformed to express a TIG2 polypeptide. In a further embodiment, a kit according to the invention can contain a polynucleotide encoding a ChemR23 polypeptide and/or a polynucleotide encoding a TIG2 polypeptide. In a still further embodiment, a kit according to the invention may comprise the specific primers useful for amplification of ChemR23 or TIG2 as described below. All kits according to the invention will comprise the stated items or combinations of items and packaging materials therefor. Kits will also include instructions for use.

EXAMPLES

In the following examples, all chemicals are obtained from Sigma, unless stated. The cell culture media are from Gibco BRL and the peptides are from Bachem.

Example 1: Cloning of human ChemR23 receptor.

Human ChemR23 was cloned as described in Samson et al. (1998) (SEQ ID Nos 1 and 2). As an example of one set of steps one could use to clone other ChemR23 polypeptides useful according to the invention, the method is described here. In order to clone the ChemR23 sequence, a classical cloning procedure was performed on human genomic DNA. A clone, designated HOP 102, was amplified from human genomic DNA by using degenerate oligonucleotides. HOP 102 shared 45-50% identity with fMLP and C5a receptors and somewhat lower similarities with the family of chemokine receptors. This partial clone was used as a probe to screen a human genomic library and three overlapping lambda clones were isolated. A restriction map of the clones was established and a 1.7 kb XbaI fragment was subcloned in pBS SK+ (Stratagene) and sequenced on both strands. The sequence was found to include the HOP 102 probe entirely, with 100% identity. This novel gene was named ChemR23 (GenBank Accession No. Y14838).

Amplification of coding sequence of ChemR23 resulted in a fragment of 1.1 kb. This fragment was subcloned into the pCDNA3 (Invitrogen) vector and sequenced on both strands.

Example 2: Purification of the natural ligand of ChemR23 and identification of TIG2.

Approximately one liter of a human ascitic fluid from a patient with ovarian cancer was prefiltered and then filtered successively through 0.45 and 0.22 µm Millex filters (Millipore).

In step 1, the ascite was directly loaded onto a C18 reverse-phase column (10 mm x 100 mm POROS 20 R2 beads, Applied Biosystems) pre-equilibrated with 5% CH_3CN/0.1% TFA at a flow-rate of 20 ml/min at room temperature. A 5-95% gradient of CH_3CN in 0.1% TFA was then applied with a slope of 6%/min. 5-milliliter fractions were collected, and 20 µl of each fraction was set aside and assayed for $[Ca^{2+}]$ transients in ChemR23-expressing CHO cells.

In step 2, the active fractions (approx. 10 fractions eluting between 25 and 40% CH_3CN) were pooled, adjusted at pH 5, filtered through a 20 µm Millex filter (Millipore), diluted 3-fold in acetate buffer at pH 4.8 and then applied to a cation-exchange HPLC column (Polycat 9.6 mm x 250 mm, Vydac) pre-equilibrated with acetate buffer at pH 4.8 and 4°C. A 0-1M gradient of NaCl in acetate buffer at pH 4.8 was applied with 10%/min at a flow-rate of 4 ml/min. 1-milliliter fractions were collected and a 25 µl-aliquot from each fraction was used for the $[Ca^{2+}]$ assay after desalting on a 10 kDa-cut-off membrane (Ultrafree, Millipore).

In step 3, the active fractions (eluted with approx. 700 mM NaCl) were pooled and desalted onto a 10 kDa-cut-off Ultrafree membrane to approx. 10 mM NaCl concentration. The eluates from distinct cation-exchange HPLC runs were pooled and loaded onto a second cation-exchange HPLC column (Polycat 2.1 mm x 250 mm, Vydac) pre-equilibrated with acetate buffer at pH 4.8 and 4°C. A 0-1 M gradient of NaCl in acetate buffer at pH 4.8 was applied at a flow-rate of 1 ml/min. with a slope of 2 %/min. 0.5-milliliter fractions were collected and a 20 µl-aliquot from each fraction was used for intracellular calcium assay after desalting onto a 10 kDa-cut-off Ultrafree membrane.

In step 4, the active fractions were pooled, diluted 8-fold with H_2O/0.1% H_3PO_4 and loaded onto an analytical C18 reverse-phase column (4.6 mm x 250 mm, Vydac) pre-equilibrated with 5% CH_3CN/0.1% H_3PO_4 at a flow-rate of 1 ml/min at room temperature. A 5-95% gradient of CH_3CN in 0.1% H_3PO_4 was applied with a 0.3%/min. gradient between 25 and 40% of CH_3CN. Individual UV absorption peaks (214 nm) were collected manually, and approx. 5% from each fraction volume was assayed for biological activity.

In step 5, the active peaks (approximatively 28% CH_3CN) were diluted 6-fold with H_2O/0.1% TFA and directly loaded onto a second C18 reverse-phase column (1 mm x 50 mm, Vydac) pre-equilibrated with 5% CH_3CN/0.1% TFA at a flow-rate of 0.1 ml/min. at room temperature. A 5-95% gradient of CH_3CN in 0.1% TFA was applied with a 0.3%/min. gradient between 30 and 45% of CH_3CN. The final peak was collected manually at 40% CH_3CN and analysed by mass spectrometry. 800 ml of ovarian cancer ascites fluid yielded 50 fmoles of TIG2.

The active fraction was completely dried in a speed-vac and resuspended in 10 µl of 0.1M Tris at pH 8.7. After boiling the sample during 15 min at 95°C, the sample was incubated at 37°C overnight in the presence of 250 ng of modified trypsin (Promega). The digested sample was then purified by solid-phase extraction onto a C18 ZipTip (Millipore). The eluted sample (1.5 µl in 70% CH_3CN/0.1% TFA) was applied onto a MALDI target in the presence of 120 mg/ml dihydroxy-benzoic acid matrix and then analysed on a MALDI-Q-TOF prototype (Micromass). Direct monoisotopic mass fingerprinting allowed to identify 7 tryptic peptides, i.e. 63 amino acids with a sequence recovery of 38.7%.

Table 1: Sequences of Peptides found in monoisotopic mass fingerprinting

The two peptides indicated with an asterisk were microsequenced by MS/MS fragmentation. The position of the peptides is defined in comparison with TIG2 amino acid sequence (Seq ID N° 5)

Residues #	Sequence	M + H
72-78	(K) LQQTSCR (K) [Seq Id. No. 13]	835.41
81-88	(R) DWKKPECK (V) [Seq. Id. No. 14]	1033.51
29-39*	(R) GLQVALEEFHK (H) [Seq. Id. No. 15]	1270.68
98-109	(K) CLACIKLGSEDK (V) [Seq. Id. No. 16]	1279.64
114-125*	(R) LVHCPIETQVLR (E) [Seq. Id No. 17]	1407.78
28-39	(R) RGLQVALEEFHK (H) [Seq. Id. No. 18]	1426.78
126-137	(R) EAEEHQETQCLR (V) [Seq. Id. No. 19]	1472.64

Example 3: Cloning and recombinant expression of human TIG2.

In order to clone the TIG2 sequence (Fig. 6, GenBank Accession No. Q99969) a polymerase chain reaction (PCR) was performed on kidney cDNA (Clontech Laboratories). Primers were synthesized based upon the human TIG2 sequence and were as follows:

hTig2 fw: 5' CAGGAATTCAGCATGCGACGGCTGCTGA 3' SEQ ID NO: 20
hTig2 rv: 5' GCTCTAGATTAGCTGCGGGGCAGGGCCTT 3' SEQ ID NO: 21

Amplification was performed with Qiagen Taq polymerase in the conditions described by the supplier and with the following cycles: 3 min at 94°C, 35 cycles of 1 min at 94°C, 90 sec at 58°C and 90 sec at 72°C, followed by a final incubation of 10 min at 72°C. The amplification resulted in a fragment of 500 bp containing the entire coding sequence of the Tig2 gene. This fragment was subcloned into the vector pCDNA3 (Invitrogen) for DNA sequencing analysis.

Maxiprep (Quiagen) DNA was used in transient transfections of HEK293 cells expressing large T antigen (293T) and COS-7 cells using Fugene6 in 10 cm plates. In parallel, transfections were performed in the same cell lines with the expression vector alone (Mock transfected). 24 h after transfection, the medium was replaced by 9 ml DMEM-F12, 1% BSA, and 3ml of supernatant were collected each 24h for three days (48, 72 and 96h post transfection). CHO cells were transfected with the same plasmid and transfected cells were selected with G418. The activity of the conditioned medium was verified on ChemR23 expressing cells using the aequorin assay.

Example 4. Recombinant expression of TIG2 in yeasts.

The coding sequences of human and mouse TIG2 are amplified by PCR using the following primers (Two different primers are used for amplification of 5' end of human TIG2 to take into account the different predictions of the signal peptide of this protein):

mTig2f:	5' TCTCTCGAGAAAAGAGAGGCTGAAGCTACACGTGGGACAGAGCCCGAA 3'	SEQ ID NO: 22
hTig2af:	5' TCTCTCGAGAAAAGAGAGGCTGAAGCTGGCGTCGCCGAGCTCACGGAA 3'	SEQ ID NO: 23
hTig2bf:	5' TCTCTCGAGAAAAGAGAGGCTGAAGCTGTGGGCGTCGCCGAGCTCACG 3'	SEQ ID NO: 24
mTig2r:	5' AGGGAATTCTTATTTGGTTCTCAGGGCCCT 3'	SEQ ID NO: 25
hTig2r:	5' AGGGAATTCTTAGCTGCGGGGCAGGGCCTT 3'	SEQ ID NO: 26

The amplified TIG2 sequences are cloned, sequenced and inserted in pPIC9K, a multicopy Pichia expression plasmid (InVitrogen) containing the signals directing secretion of expressed proteins. Following transformation, Pichia pastoris cells are selected using G418 antibiotic. After selection, 20 clones are analyzed for their expression and the clone with the highest expression is amplified for large scale expression in shaker flasks. The medium is collected, centrifuged and used for partial purification with a protocol derived from the one used for TIG2 initial purification (see above).

Example 5. Recombinant expression of chimaeric TIG2 fused with Secreted Alkaline Phosphatase (SEAP).

The coding sequences of mouse and human TIG2 are amplified by PCR, cloned and sequenced. PCR and sequencing primers are as follows:

mTig2f:	CAGGAATTCGCCATGAAGTGCTTGCTGA	(SEQ ID NO: 27)
hTig2f:	CAGGAATTCAGCATGCGACGGCTGCTGA	(SEQ ID NO: 28)
mTig2r:	GCTCTAGATTTGGTTCTCAGGGCCCTGGA	(SEQ ID NO: 29)
hTig2r:	GCTCTAGAGCTGCGGGGCAGGGCCTTGGA	(SEQ ID NO: 30)

The cloned TIG2 sequences are then subcloned into the mammalian bicistronic expression vector, pEFIN, to obtain a fusion protein with TIG2 linked at its carboxy terminal end to secreted alkaline phosphatase, tagged with six histidine residues (His6). Mammalian cells, including COS-7, HEK-293 expressing the large T antigen (293 T) and CHO-K1 cells, are transfected with this plasmid using Fugene 6™ and incubated for 3-4 days in complete Ham's F12 medium (Nutrient Mixture Ham's F12 (Life Technologies) containing 10% fetal bovine serum; 100 IU/ml penicillin, 100 µg/ml streptomycin and 2.5 µg/ml fungizone (Amphotericin B). The supernatant containing TIG2-SEAP-His6 is collected after centrifugation, filtered (0.45 µm) and stored at 4°C after adding 20 mM Hepes (pH 7.4) and 0.02% sodium azide.

For one-step affinity purification of the TIG2 fusion protein, the supernatant is applied to 1 ml of Hisbond resin (Qiagen). After washing, bound TIG2-SEAP-His6 is eluted with a gradient of imidazol. The concentration of isolated TIG2-SEAP-His6 is determined by a sandwich type enzyme-linked immunosorbent assay. Briefly microtiter plates are coated with anti-placental alkaline phosphatase antibody. After blocking with 1 mg/ml bovine serum albumin (BSA) in phosphate buffered saline, the samples are titrated and incubated for 1 h at room temperature. After washing, plates are incubated with biotinylated rabbit anti-placental alkaline phosphatase diluted 1:500 for 1 h at room temperature, washed again, and incubated with peroxidase-conjugated streptavidin for 30 min. After washing, bound peroxidase is reacted with 3, 3',5,5'-tetramethylbenzidine. The reaction is stopped by adding 1 N H_2SO_4, and absorbance at 450 nm is measured. Alkaline phosphatase activity is determined by a chemiluminescent assay using the Great Escape™ detection kit (Clontech). Purified placental alkaline phophatase is used to generate a standard curve. The enzymatic activity is expressed as relative light units/sec.

Example 6: Functional assay for ChemR23.

ChemR23 expressing clones have been obtained by transfection of CHO-K1 cells to coexpressing mitochondrial apoaequorin and Gα16, limiting dilution and selection by northern blotting. Positive clones were used for screening with human ovarian cancer ascites extracts prepared as described above. A functional assay based on the luminescence of mitochondrial aequorin intracellular Ca^{2+} release (Stables et al., 1997, Anal. Biochem. 252:115-126; incorporated herein by reference) was performed as described (Detheux et al., 2000, J. Exp.

Med., 192 1501-1508; incorporated herein by reference). Briefly, cells were collected from plates in PBS containing 5 mM EDTA, pelleted and resuspended at 5 x 10^6 cells/ml in DMEM-F12 medium. Cells were incubated with 5 µM Coelenterazine H (Molecular Probes) for 4 hours at room temperature. Cells were then washed in DMEM-F12 medium and resuspended at a concentration of 0.5 x 10^6 cells/ml. Cells were then mixed with test agonist peptides or plates containing tissue extracts and the light emission was recorded for 30 sec using a Microlumat luminometer (Perkin Elmer). Results are expressed as Relative Light Units (RLU).

Example 7: Activation of cells expressing ChemR23 by recombinant TIG2.

The conditioned medium of COS-7, CHO-K1 and 293 T cells transfected with pCDNA3 encoding TIG2 or pCDNA3 alone, was collected and used for aequorin assays on CHO cells expressing ChemR23. Results are shown in Figure 12. Increasing amounts of conditioned supernatant resulted in an increase in luminescence in aequorin system cells expressing ChemR23.

Example 8: Production of antibodies specific for ChemR23.

Antibodies directed against ChemR23 were produced by repeated injections of plasmids encoding ChemR23 into mice. Sera were collected starting after the second injection and the titre and specificity of the antibodies was assessed by flow cytofluorometry with CHO-K1 cells transfected with the ChemR23 cDNA and CHO-K1 cells transfected with the cDNA of unrelated GPCR cDNA. Several sera were positive and were used for immunohistochemistry and other related applications, including flow cytometry analysis of human primary cells.

Monoclonal antibodies were obtained from immune mice by standard hybridoma technology using the NSO murine myeloma cell line as immortal partner. Supernatants were tested for anti ChemR23 antibody activity using the test used for assessing the antisera. Cells from the positive wells were expanded and frozen and the supernatants collected.

Figure 13 shows the results of experiments to characterize the antibodies raised against ChemR23. A mixture of recombinant cells made up of 2/3 recombinant ChemR23 CHO cells and 1/3 mock-transfected CHO cells (negative control) was reacted with either a supernatant of cells expressing the anti ChemR23 5C 1H2 monoclonal antibody (thick line) or a supernatant

from cells with no known antibody activity (thin line, grey filling). After staining with FITC labeled anti mouse Ig these preparations were analyzed by flow cytofluorometry. Results are displayed as a histogram of the number of cells (Events axis) expressing a given fluorescence (FL1-H axis). Monoclonal 5C 1H2 allowed the discrimination of the ChemR23 recombinant sub-population of cells from the negative control cells, as evidenced by the relative proportions of both types of cells. The background fluorescence of the assay is given by the second staining (grey filling).

Example 9. Binding displacement assay.

For displacement experiments, ChemR23-CHO-K1 cells (25,000 cells/tube) are incubated for 90 min. at 27°C with 1 nM of SEAP-HIS6 or TIG2-SEAP-HIS6 in the presence of increasing concentrations of unlabeled TIG2 in 250 µl of binding buffer (50 mM Hepes pH 7.4; 1 mM Ca Cl_2; 0.5% Bovine Serum Albumin (BSA) Fatty Acid-Free; 5 mM $MgCl_2$). For saturation experiments, ChemR23-CHO-K1 cells (25,000 cells/tube) are incubated for 90 min at 27°C with increasing concentrations of TIG2-SEAP-HIS6 in the presence or absence of 1 µM unlabeled TIG2. After incubation, cells are washed 5 times and lysed in 50 µl of 10 mM Tris-HCl (pH 8.0), 1% triton X100. Samples are heated at 65°C for 10 min to inactivate cellular phosphatases. Lysates are collected by centrifugation, and alkaline phosphatase activity in 25 µl of lysate is determined by the chemiluminescence assay described above.